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ALIGNMENTS

BASE COUNT ORIGIN	FEATURES Source	TITLE I	AUTHORS 1	REFERENCE			SION	A70382 LOCUS
/organism="unidentified" /db_xref="taxon:32644" 336 a 541 c 453 g 299 t	Location/Qualifiers 1. 1629	A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME PACENT: WO 9811225-A 19-MAR-1998; NICOLA NICOS ANTOWY (AI)	Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S., Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and Kikuchi,Y.	unidentified unclassified. 1 (bases 1 to 1629)	unidentified.	94774663 A70382.1 GI:4774663	ent	A70382 1629 bp DNA
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                                            A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC PATENT: WO 9811225-A 19-MAR-1998; NICOLA NICOSA ANTONY (AU)

Location/Qualifiers
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NICOLA,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda, Kikuchi,Y.
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2 (bases 1 to 1716)
Elson, G.C.A., Graber, P., Losberger, P., Herren,
Menoud, L.N., Wells, T.N.C., Kosco-Vilbols, M.H.
Direct Submission
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AAGAACATGAAGGACTTGACCTGCCGCTGGACGCCAGGGGGCCCACGGGGGAGACCTTCCTC
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                                                                                                    tccaggcagcagtcaggagacaatctggtgtgtcacgcccgagacggcagcagtctggct 507
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Sequence
A70393
94774671
A70393.1
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Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,
Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
Kikuchi,Y.
                                                                                                                                                                                                                                                                                unidentified
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                                                                                                                           Similarity 88.(
93; Conservative
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Location/Qualifiers
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/db_xref="taxon:32644"
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Pred. No. 6.5e-85;
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               gcgggaatctggagcgagtggagccaccccaccgctgcctccaccccttgaagtgagcgc 116]
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Sequence 16 from Patent W
A70386
4774665
A70386.1 GI:4774665
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Nicola,N.A., Fabri,L., Farley,A.,
Zhang,J., Alexander,W., Hilton,D.
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ilarity 100.0%;
Conservative (
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GKLGEACVGGKGAEEERDPGEQPPQHRTLLSKHRTRGSCPRADGVRREVRGSG"
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0; Mismatches 0;
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                                                                  GAGACGGCAGCATTCTGGCTGGCTCCTGCCTCTATGTTGGCT
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Sequence
A70398
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Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S., Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and Kikuchi,Y.
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94774683
A70408.1
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                                                                                                                                                                                                                                                g2636669
AC0031·12.1
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Kikuchi,Y.
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Nicola, N.A., Fabri, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unidentified
                                                                                                                                                                                                                                                                                       AC003112 40668 bp DNA
Human DNA from chromosome 19
sequence, complete sequence.
                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 4068)

Lamerdin,J.E., McCready,P.M., Adamson,A.W., Burkhart-Schultz,K., Gordon,L., Christensen,M., Kyle,A., Ramirez,M., Stilwagen,S., Garnes,J., Danganan,L., Bruce,B., Quan,G., Montgomery,M., Ow,D., Kobayashi,A., Olsen,A.O. and Carrano,A.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
Lamerdin, J.E.
Direct Submission
Submitted (21-NOV-1997) Hu
National Laboratory, 7000
                                                                                                                                                                                                          Homo sapiens
                                                       Unpublished
2 (bases 1 to
                                                                                               Sequence analysis
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/db_xref="taxon:32644"
1 3367 c 3298 g 272
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99.6%;
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Pred. No. 4.9e-49;
  Human Genome
00 East Ave.,
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R30292, genomic
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                                                                                                                                                 misc_feature
                                                                                                                                                                frame: 1, quality: excellent, score: 100.000-DDS similarity to AA047548 zf15e02.rl Soares fetal heart NbH119W Homo sapiens cDNA clone 377018 5' (139. 221); 100% identity. -DDS similarity to AA136115 z490b04.rl Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490063 5' (111. 192); 99% identity. -DDS similarity to AA452628 zx33f04.rl Soares total fetus NbHFB 9w Homo sapiens cDNA clone 788287 5' (83. .165); 100% identity. -DDS similarity to AA009412 ze82h02.rl Soares fetal heart NbHH19w Homo sapiens cDNA clone 365523 5' (62. .144); 100% identity."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"DDS similarity to AA047548 zf15e02.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone 377018 5′ (1. .138); 96% identity. ~-Other overlapping matches: ~(10435. .10548) DDS similarity to AA136115 zk90b04.rl Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490063 5′ (1. .110); 93% identity. ~~(10466. .10548) DDS similarity to AA452628 zx33f04.rl Soares total fetus Nb2HFB 9w Homo sapiens cDNA clone 788287 5′ (1. .82); 95% identity. ~~(10486. .10548) DDS similarity to AA009412 ze82h02.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone 365523 5′ (1. .61); 97%
/note-"DDS similarity to AA136115 zk90b04.rl Soares /note-"DDS similarity to AA136115 zk90b04.rl Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490063 5/ (133. 394); 94% identity.--DDS similarity to AA009412 ze82h02.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone 365523 5' (145. .346); 96% identity.--(11121. .11:
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/note="predicted exon,
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/rpt_family="Alu"
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/rpt_family="Alu"
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/note="LL19NC03 cosmid library constructed at LLNL from
flow-sorted chromosomes from hybrid 5HL2-B, which carries
chromosome 19 as its only human chromosome."
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._family="Alu"
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e="predicted exon, program: grail2exons_human_1.3,
e=: 1, quality: excellent, score: 75.000"
lement(9288. .10123)
family="Alu"
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_line="5HL2-B"
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"predicted exon, |
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predicted exon,
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d, score: 62.000"
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Inotes DDS similarity to AA406406 zv11e07.sl Soares NhHMPu Sl Homo sapiens cDNA clone 75338 3′ (1. 433); Score: 858 Identity: 431/433 (99%).--(14884. 1.15237) DDS similarity to W37175 zb21a02.rl Soares fetal lung NbHL19W Homo sapiens cDNA clone 302666 5′ (1. .355); 94% identity.--(15227. .14885) DDS similarity to AA121532 zk89c11.sl Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490004 3′ (342. .1); 99% identity.--(15227. .14885) DDS similarity to AA127694 zk89c11.rl Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490004 5′ (126. .467); 99% identity.--(15227. .14997) DDS similarity to W46603 zc32h10.rl Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 324067 5 (328. .1); 98% identity.--(15227. .15088) DDS similarity to W46604 zc32h10.sl Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 324067 3′ (322. .465); 96% identity."
                                                 /note-*DDS similarity to AA121532 zk89c11.s1 Soares /note-*DDS similarity to AA121532 zk89c11.s1 Soares pregnant uterus NbHPU Homo saplens cDNA clone 490004 3' (389. .343); 99% identity.--DDS similarity to AA127694 zk89c11.r1 Soares pregnant uterus NbHPU Homo saplens cDNA clone 490004 5' (77. .125); 90% identity.--(15735. .15713) DDS similarity to W46603 zc32h10.r1 Soares senescent fibroblasts NbHSF Homo saplens cDNA clone 324067 5' (351. .329); 100% identity.--(15735. .15713) DDS similarity to W46604 zc32h10.s1 Soares senescent fibroblasts NbHSF Homo saplens cDNA clone 324067 3' (299. .321); 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"predicted exon, program: grail2exons_human_1.3, frame: 2, quality: good, score: 61.000--Other overlapping matches:-(13756. 13826) DDS similarity to AA009412 ze82h02.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 365523 5' (428. 496); 97% identity.--(13756. 13984) DDS similarity to AA009693 ze82h02.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 365523 3' (227. 1); 98% identity.--(13756. 13984) DDS similarity to AA450010 zx33f04.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 788287 3' (228. 1); 99% identity.--"
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/rpt_family="Alu"
14885...15317
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/rpt_family="Alu"
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complement(15895.
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/note="DDS similarity to AA136115 zk90b04.rl Soares
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    .16082)
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/note="predicted exon, program: grail2exons_human_1.3, frame: 0, quality: excellent, score: 81.000~-Other overlapping matches:~(15936. .15895) DDS similarity to

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REFERENCE
AUTHORS
TITLE
                                                                                                                                                            SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                    DEFINITION
                          FEATURES
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  1 (bases 1 to 7218)
Dorner,F., Scheiflinger,F. and Falkner,F.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
Location/Qualifiers
1. .7218
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8; Conserv
                                                                                                   McGeoch,D.J., Dalrymple,M.A., Davison,A.J., Dolan,A., Frame,M.C., McNab,D., Perry,L.J., Scott,J.E. and Taylor,P.
The complete DNA sequence of the long unique region in the genome of herpes simplex virus type 1
J. Gen. Virol. 69 (Pt 7), 1531-1574 (1988)
                                                                                                                                                                               submitted (17-JAN-1989) McGeoch D.J., Institute of Virology, Church Street, Revised by [7] 2 (bases 9001 to 117360)
                                                                                                                                                                                                                                                                                                                                                 capsid protein; complete genome; desoxyribonuclease; desoxyuridine triphosphatase; DNA polymerae; brinding protein; kinase; long terminal repeat; origin of replication; regulatory protein; repetitive sequence; ribonucleotide reductase; tegument protein; thymidine kinase.
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Herpes simplex virus
X14112 D00317 D00374
           Perry,L.J. and McGeoch,D.J.

The DNA sequences of the long repeat region and adjoin:
the long unique region in the genome of herpes simplex
J. Gen. Virol. 69 (Pt 11), 2831-2846 (1988)
                                                                                                                                                                                                                                                                        Viruses; dsDNA viruses, no RNA stage; Alphaherpesvirinae; Simplexvirus.
1 (bases 1 to 152261)
                                                                                                                                                                                                                                                                                                                      human herpesvirus
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McGeoch,D.J., Dolan,A., Donald,S. and Rixon,F.J.
Sequence determination and genetic content of the short unique
region in the genome of herpes simplex virus type 1
Mol. Biol. 181 (1), 1-13 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-APR-1997) Dolan A., MRC Virology Institute, Institute of Virology, Church Street, Glasgow Gll 5JR, GB on Apr 18, 1997 this sequence version replaced gi:59499.

See also x06461 and x02138.

Residues 1 - 8661 and 148674 - 152260 of TR-L and TR-S, resp. have not been sequenced but are derived from IR-L and IR-S sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism∞"human herpesvirus 1"
/strain="17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAPPPPPAGGPPPSCSLLLROWLHVPESASDDDDDDDDDDDDDPPPEPAPEARPTAAAPR
PRPPPPGVGPGGGADPSHPPSRPFRLPPRLALRLRVTAEHLARLRLRRAGGEGAPEPP
ATPATPATPATPATPARVRFSPHVRVRHLVVWASAARLARRGSWARERADRARFRRRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="neurovirulence
/protein_id="CAA32348.1"
/db_xref="PID:e312308"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
/db_xref="SWISS-PROT: P08393"

/translation="MEPRPGASTRRPEEGPOREDAPDVWVFPCDRDLPDSSDSEAETE
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PPREDGSDEGTVCAVCTDEIAPHLRCDTFPCMHRFCIPCMCTMWQRFAPRXLTLGGH
VYLIVGVTPSGSFSTIPIVNDPQTRMEAEEAVRAGTAVDFIWTGNQRFAPRXLTLGGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="a sequence(terminal redundancy)"
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                                                                                                                                                                                                                                                         <sub>J</sub>∪ın(2261. .2317,3083. .3749,3886.
'gene≖"RL2"
                                                                                                                                                                                                                                                                                                                                                                                  /note="reiteration set 6"
1534. .1539
                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="RL1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref-"SPTREMBL:012396"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="PID:g1944537"
/db_xref="GI:1944537"
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                                                                                                                                                                /protein_id="CAA32336.1"
/db_xref="PID:e312309"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EAEAVIGPCLGPEARARALARGAGPANSV"
                                                                                                                                          /db_xref="PID:g59500"
                                                                                                                                                                                                                 codon_start=
                                                                                                                                                                                                                                     function="modulator of cell state and gene expression"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       reiteration set 7"
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ASTETRPGSGGEPAACRSSGPAALLAALEAGPAGVTFSSSAPPDPPMDLTNGGVSPAA TSAPLDWTTFRRVFLIDDAWRPLMEPELANPLTAHLLAEYNRRCQTESVLPPREDVFS WTRYCTPDEVRVVIIGQDPYHHPGQAHGLAFSVRANVPPPPSLRNVLAAVKNCYFEAR

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EAEAGRPRGRTGPLYNRPAPLANNRDPTVISDSPPASPHRPPAAPMPGSAPRPGPPAS
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EQSLCRARATVARGSGGPGVEGGHGPSRGAAPSGAAPLPSAASVEQEAAVRPRKRRGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="RL2"
5676. .5681
/gene="RL2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GQENPSPQSTRPPLAPAGAKRAATHPPSDSGPGGRGQGGPGTPLTSSAASASSSSASS
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                                                                                                                                                                                                                                                                                     VPLPSDDLDWRYETPSAINYALIDGIELRYHOPGLDTVLWDRHAQKAYWVNPELFVAG
FLEDLSYPAFPANTQETETRLALYKEIRQALDSRKQAASHTPVKAGCVNFDYSRTRRC
VGRQDLGPTNGTSGRTPVLPPDDEAGLQPKPLTTPPPIIATSDPTPRRDAATKSRRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8806. .8826
/gene="RL2"
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032. 9212
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'note="reiteration
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)337. .10011
                                                            /protein_id="CAA32338...
/db_xref="PID:e312316"
/db_xref="PID:959503"
                                                                                                                                                                                                                                                                                                                                                                             db_xref="GI:59502"
db_xref="SWISS-PROT:P10185"
                                                                                                                                                                                                                                                                                                                                                                                                                                     protein_id="CAA32337.1"
protein_id="CAA32337.1"
ib_xref="piD:e312315"
ib_vref="piD:e312315"
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                    db_xref="SWISS-PROT:P10186"
                                         db_xref="GI:59503"
                                                                                                                                 product-"uracil-DNA glycosylase"
                                                                                                                                                                                                                         gene-"UL2"
                                                                                                                                                                                                                                                                                                                                                             translation="MGILGWVGLIAVGVLCVRGGLPSTEYVIRSRVAREVGDILKVPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
translation="MKRACSRSPSPRRRPSSPRRTPPRDGTPPQKADADDPTPGASND
                                                                                                                                                                               gene="UL2"
                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="PID:g59502"
                                                                                                                                                    codon_start=1
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                                                                                                                                                                                                                                                                     [SRRL"
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Best Local Similarity
Matches 91; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ccgccgcggccgctgtcctcgctgtggtcgcctc 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  capsid protein; complete genome; desoxyribonuclease; desoxyuridine triphosphatase; DNA polymerase; DNA-binding protein; genome; glycoprotein; kinase; long terminal repeat; origin of replication; regulatory protein; repetitive sequence; ribonucleotide reductase; tegument protein; thymidine kinase.
   3 (bases 113322 to 126373)
Perry.L.J. and McGeoch,D.J.
The DNA sequences of the long repeat region and adjoining parts of the long unique region in the genome of herpes simplex virus type of the long unique region in the genome of herpes simplex virus type of the long unique region in the genome of herpes simplex virus type of the long unique region in the genome of herpes simplex virus type of the long unique region in the genome of herpes simplex virus type of the long unique region in the genome of herpes simplex virus type of the long unique region in the genome of herpes simplex virus type of the long unique region in the genome of herpes simplex virus type of the long unique region in the genome of herpes simplex virus type of the long unique region in the genome of herpes simplex virus type of the long unique region in the genome of herpes simplex virus type of the long unique region in the genome of herpes simplex virus type of the long unique region in the genome of herpes simplex virus type of the long unique region in the genome of herpes simplex virus type of the long unique region in the genome of herpes simplex virus type of the long unique region in the genome of herpes simplex virus type of the long unique region in the genome of herpes simplex virus type of the long unique region in the genome of herpes simplex virus type of the long unique region in the genome of herpes simplex virus type of the long unique region in the long unique
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(Chases 9001 to 117360)

McGeoch,D.J., Dalrymple,M.A., Davison,A.J., Dolan,A., Frame,M.C., McGeoch,D.J., Dalrymple,M.A., E and Taylor,P.

The complete DNA sequence of the long unique region in the genome of herpes simplex virus type 1

J. Gen. Virol. 69 (Pt 7), 1531-1574 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses, dsDNA viruses, no RNA stage; Alphaherpesvirinae; Simplexvirus.
1 (bases 1 to 152261)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human herpesvirus 1 human herpesvirus 1
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Herpes simplex virus
X14112 D00317 D00374
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (17-JAN-1989) McGeoch D.J., Institute of Virology, Church Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McGeoch, D.J
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10957
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/gene="RL2"
complement(11753 . .11758)
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/translation="MYKPLVSYGSVMSGVGEGGVPSALAILASWGWTFDTPNHESGIS
PDTTPADSIRGAAVASPOPLHGGPEREATAPSFSPTRADDGPPCTDGPYVTFDTLFM
VSSIDELGRRQITDTIKDLRLSLAKFSIÄCTKTSSFSGNAPRHHRRGAFQRGTEAPR
VSSIDELGRRQITDTIKDLRLSLAKFSIÄCTKTSSFSGNAPRHFYGSFVFVHEFVSS
SNKSLOMFVLCKRAHAARVREQLRVVIQSRKPRKYYTRSSDGRLCPAVPVFVHEFVSS
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10957
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/db_xref="PID:e312317"
/db_xref="PID:g59504"
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(HSV) type 1 complete
S40593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                MRC Virology Institute, Glasgow Gll 5JR; GB
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85160822
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McGeoch, D.J., Dolan, A., Donald, S. and Rixon, F.J.

Sequence determination and genetic content of the short unique region in the genome of herpes simplex virus type 1

J. Mol. Biol. 181 (1), 1-13 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of Virology, Church Street, Glasgow G11 5JR, GE On Apr 18, 1997 this sequence version replaced See also x06461 and x02138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dolan,A., McKie,E., MacLean,A.R. and McGeoch,D.J. Status of the ICP34.5 gene in herpes simplex virus type 1 J. Gen. Virol. 73 (Pt 4), 971-973 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McGeoch,D.J., Dolan,A., Donald,S. and Brauer,D.H. Complete DNA sequence of the short repeat region herpes simplex virus type 1
Nucleic Acids Res. 14 (4), 1727-1745 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-APR-1997) Dolan A., MRC Virology Institute, of Virology, Church Street, Glasgow G11 5JR, GB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 - 8661 and 148674 - 152260 of TR-L and TR-S,
/db_xref="SWISS-PROT:P08393"
/translation="MEPREGASTREPEGREPAPDVWVFPCDRDLPDSSDSEAETE
VGGRGDADHHDDDSASEDSTDTELFETGLLGPQGVDGGAVSGGSPPREEDPGSCGGA
PPREDGGSDEGDVCAVCTDELAPHLRCDTFPCMHRFCLPCMKTMMQLRWTCPLCNAKL
VYLIVGVTPSGSFSTIPIVNDPQTRMEAEEAVRAGTAVDFIWTGNQRFAPRYLTLGGH
                                                                                                                                                                                                                                                                                                                        /note="reiteration 1534. .1539
                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MarrrhrgprprppgptgavptaQSQVTSTPNSEPAVRSAPA
AAPPPPPAGGPPSCSLLLRQWLHVPESASDDDDDDDDDDDDDPPEPAPEARPTAAAPR
PRPPPPGVGPGGGADPSHPPSRPFRLPPRLALRLRVTAEHLARLRLRRAGGEGAPEPP
                                                                                                /protein_id="CAA32336.1"
/db_xref="PID:e312309"
/db_xref="PID:959500"
/db_xref="GI:59500"
                                                                                                                                                                                                                                                                                                                                                                                                       AEAEAVIGPCLGPEARARALARGAGPANSV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="human herpesvirus
/strain="17"
                                                                                                                                                                                                                                                                                                                                                                                                                              at pat pat pat par parvrf s phvrvrhlvvwasaarlarrg swareradrarfrrrv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="PID:e312308"
/db_xref="PID:g1944537"
/db_xref="GI:1944537"
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                                                                                                                                                                                                                                                               /gene="RL2"
                                                                                                                                                                                                                                                                                                   gene="RL1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="neurovirulence
/protein_id="CAA32348.1"
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                                                                                                                                                                                  codon_start=
                                                                                                                                                                                                                                            oin(2261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="reiteration set
                                                                                                                                                                                                                     oin(2261. .2317,3083. .3749,3886. .5489)
pene="RL2"
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                         ASTETRPGSGGEPAACRSSGPAALLAALEAGPAGVTESSSAPPDPPMDLTNGGVSPAA
TSAPLDWTTFRRVFLIDDAWRPLMEPELANPLTAHLLAEYNRRCQTEEVLPPREDVFS
WTRYCTPDEVRVVIIGODPYHHPGQAHGLAFSVRANVPPPPSLRNVLAAVKNCYPEAR
MSGHGCLEKWARDGVLLLNTTLTVKRGAAASHSRIGWDRFVGGVIRRLAARRPGLVFM
LWGTHAQNAIRPDPRVHCVLKFSHPSPLSKVPFGTCQHFLVANRYLETRSISPIDWSV
                                                                                                                                                                                                                      /product = uracil - DNA glycosylase "
/protein_id = "CAA32338.l"
/db_xref = "PID:e312316"
/db_xref = "PID:959503"
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FLEDLSYPAFPANTQETETRLALYKBIRQALDSRKQAASHTPVKAGCVNFDYSRTRRC
                                                                                                                                                                                                                                                                                                                                                                  984. .10888
gene="UL2"
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PAAARTAPPSAPIGPHGSSNTNTTTNSSGGGGSRQSRAAAPRGASGPSGGVGVGVGVV
EAEAGRPRGRTGELVNRPAPLANNRDDIVISDSPPASPHRPPAAPMPGSAPRPGPPAS
EAAASGPARPRAAVAPCVRAPPPGGPGPRAPAPGAEPAARPADARRVPQSHSSLAQAANQ
                                                                                                                                 translation="MKRACSRSPSPRRRPSSPRRTPPRDGTPPQKADADDPTPGASND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'product="virion glycoprotein L"
'protein_id="CAA32337.1"
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/gene="RL2"
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                                                                                                                                                                      db_xref="SWISS-PROT:P10186"
                                                                                                                                                                                                     db_xref="GI:59503"
                                                                                                                                                                                                                                                                                                                                 codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="5'end of stable LAT (latency associated transcript)
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ORGANISM
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                                                                                                                                                                                           FEATURES
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Best Local
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l Similarity 59.1%;
91; Conservation
                                                                                                                                                                                                                                    Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Simplexvirus.

1 (bases 1 to 6633)

McGeoch, D.J., Dolan, A., Donald, S. and Brauer, D.H. Complete DNA sequence of the short repeat region in herpes simplex virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                           TEHSVIOS 0633 bp DNA VRL 30-APR-1996 Herpes simplex virus type I immediate early (IE) gene 3 for transcriptional activator IE175 (= ICP 4).
                                                                                                                                                                                                                                                                                                                                   human herpesvirus 1 human herpesvirus 1
                                                                                                                                                                                                                                                                                                                                                                 IE gene 3; IE175 protein;
transcriptional activator.
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10957.
                                                            /map="R(s) region"

complement(<1...479)

/note="primary transcript of IE68

complement(<1...64)
                           /note="Exon 1 IE68" complement(65. 232)
complement(113.
                                                                                                                       /organism="human herpesvirus
/strain="17"
/db_xref="taxon:10298"
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                                                                                                                                                                                        Location/Qualifiers
                'note="Intron
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/gene="RL2"
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11715. .11720
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VSSIDELGRRQLTDTIRKDLRLSLAKFSIACTKTSSFSGNAPRHHRRGAFQRGTRAPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "translation="MVKPLVSYGSVMSGVGGEGVPSALAILASWGWTFDTPNHESGIS
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/db_xref="PID:e312317"
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db_xref="GI:59504
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.217)
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Best Local Similarity 59.1%;
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5463..5795
/note="repetitious region 2"
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/note="repetitious region 3"
6232..>6232
/note="a' sequence"
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/note="Exon 2 IE68"
complement(502. .509)
/note="TATA-Box (IE68 gene)"
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NPRVVPGDVALDQACFRISGAARNSSSFITGSYARAVPHLGYAMAAGRFGWGLAHAAA
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complement(233. .479)
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/note="repetitious region 4"
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>_xref="PID:g59849"
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hte="IE175 mRNA"
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anslation="MASENKQRPGSPGPTDGPPPTPSPDRDERGALGWGAETEEGGDD
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/5D_COMB.seq:*
/cgn2_6/ptodata/2/ina/DCTUS9_COMB.seq:*
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US-08-728-259A-10
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US-08-520-678A-30
PCT-US96-00419-4
US-08-08-52-122-12
US-08-085-122-12
US-08-184-237-5
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US-07-928-611-12

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US-08-487-811A-12

US-08-487-811A-21

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PCT-US93-07370-16

US-08-623-471-8

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US-08-850-392-
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7 33 cgcgtgcggacccgagccccaatctgcaccccgcagactcgccccagccccataccggcc	Query Match 3.3%; Score 53.6; DB 2; Length Best Local Similarity 2.1%; Pred. No. 0.0023; Matches 8; Conservative 225; Mismatches 149; Indel	ALIGNMENTS RESULT 1 US-08-232-463-14 Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION: RECOMBINANT FOWLPOX VIRUS APPLICANT: SCHEIFLINGER, F. APPLICANT: RALKMER, F. APPLICANT: RESONBERS CORRESSEE: FOLEY & Lardner STRIE: 1800 Diagonal Road, Suite 500 CITY: Alexandria COUNTRY: USA ZIF: 22313-0399 COMPUTER READABLE FORM: MEDIUM TYPE: FLOPY disk COMPUTER IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTMARE: PRESCENTION DATA: MEDIUM TYPE: FLOPY disk COMPUTER SAPLICATION NUMBER: US/08/232,463 FILING DATE: SOFTMARE: PARCHETINGERS: US/08/232,463 FILING DATE: 105/08/232,463 FILING DATE: 26 AUG-193 APPLICATION NUMBER: US/08/232,463 FILING DATE: 26 AUG-193 APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELEPHONE: (703)836-9300 FILEX: 899149 INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 7218 base pairs TYPE: nucleic acid STRANDEDNESS: Single CLONE: PTSPCT-FIS US-08-232-463-14	38 41 2.5 2884 1 US-08-148-209A-5 39 41 2.5 198 3 US-08-330-108-16 40 41 2.5 1364 4 US-08-872-302-3 41 41 2.5 198 5 PCT-US92-10087-16 42 40.8 2.5 3047 2 US-07-927-851-2 43 40.8 2.5 6671 2 US-08-280-443-1 44 40.8 2.5 1687 2 US-08-143-219-26 45 40.8 2.5 3047 2 US-08-453-323-2
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NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
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OLECULE TYPE: DN
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NAME: Leary Ph.D., Kathryn R.
REGISTRATION NUMBER: 36,317
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                 ORGANISM:
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Herpes Simplex Virus Type 1

    Woodcock, Washburn, Kurtz, Mackiewicz & No. 5821339ris
    One Liberty Place, 46th floor

                                                                                                                                     12001 base pairs
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                 Herpes simplex virus
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SYSTEM: PC-DOS/MS-DOS
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                                                                           DNA (genomic)
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                                                                                                                                                                                               568-3100
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2777 AGGGCCCCGACCCCCTGGGCGGCTGGCGGCGGCAGCCCCGGGGGCCCAGCCACACGGCGG.2836

109 ttgcgcgccacccccatgcccgcgggtcgcccggggcccgtcgcccaatccgcgcgggggg 168

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Sequence 1, AFF-
No. 587692
                                  Matches
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Re
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                          TYPE: nuclei
STRANDEDNESS:
                                                                                                                                                                                                                                                                              FILING DATE: 2
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
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                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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ccccaatctgcaccccgcagactcgcccccccccataccggcgttgcagtcaccgcccg 108
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1: USA
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                                                                                                                                                4257 base pairs
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О.
                                   Conservative
                                                                                                                                                                                                                             DOCKET NUMBER:
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                              Score 53.2; Db 4;
Pred. No. 0.0024;
"" ematches 63;
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                                                         Length 4257;
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US-08-056-051-5
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Best Local :
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INFORMATION FOR SEQ ID NO:
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NAME: NO. 5516683nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1092-C
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APPLICATION NUMBER: US
FILING DATE: 19930429
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                            FEATURE:
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Local
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merex: 910-221-5317
                                                       65 gcagactcgccccccccccataccggcgttgcagtcaccgccgttgcgcccgttgcgcccccta 124
                                                                                                                                                                                                                                                                                     NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                           1610 base pairs
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10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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James R
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                                                                                                                                               Score 49.8; DB Pred. No. 0.01; 0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 803 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 cccacacagetgtaatcagecccaggaecccaecetteteateggeteeteetgeaag
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OPERATING SYSTEM:
                                                                                                                                                                                                                                            OTHER
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                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                     IDENTIFICATION METHOD: experimental SITE INFORMATION: /function= "PstI site" THER INFORMATION: /evidence= EXPERIMENTAL
                                                                                                                NAME/KEY: misc_feature 
LOCATION: 257..262
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                                                                                                                                                                             /evidence= EXPERIMENTAL
/standard_name= "Alternate Exon 3: D4.7"
/note= "This sequence represents the third exon
allele D4.7 of the human D4 dopamine receptor
                                                                                                                                                                 gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/07/928,611
                                    'standard_name= "PstI site"
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"This sequence is a PstI site whereby
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Matches 144;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
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STATE: Illinois
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            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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compatible
                                                                                          Wacker Drive
                                                                                                                                                                      Olivier
                                                                                                                                                         Hubert
                                                                                                                                            ubert H.M. 
No. 5883226el
                                                                                                       Boehnen Hulbert & Berghoff
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lR: 90,1092-в
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                                                                                                                                          Human Dopamine Receptor and Uses
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US-08-487-811A-12
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Best Local Similarity
Matches, 144; Conserv
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SEQUENCE CHARACTERISTICS:
LENGTH: 803 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: FEATURE:
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TELECOMMUNICATION INFORMATION: 312-913-0001
                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                        125
                                                                                             450 CCGGCCTCCCCCGGACCCCTGCGGCCCCGACTGTGCGCCCCCGCGCCCCGGCCTCCCCC 509
185 cctcgctgtggtcgcctctgttgctctgtgtcctcggggtgcctcggggcggatcgggag 244
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SOFTWARE: Patent
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                                AGGACCCCTGCGGCCCGACTGTGCGCCCCCCCGCCCCGGCCTTCCCCGGGGTCCCTGCG 569
                                                              tgcccgcgggtcgcccgggccccgtcgcccaatccgcgcggcggccgccgccgccgctgt 184
                                                                                                                                                                               cgagcttcgctgtccgcgcccagtgacgcgcgtgcggacccgagccccaatctgcacccc 64
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NO. 5883226nan, Kevi...
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ilarity 47.8%;
Conservative
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Release #1.0, Version #1.25
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/note= "This sequence is a PstI site whereby
digestion of human genomic DNA produces a RFLP"
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allele
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/note= "This sequence is a repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                     /evidence- EXPERIMENTAL
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/rpt_type= "tandem"
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/standard_name= "Alternate Exon 3: D4.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               function= "PstI site"
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Pred. No. 0.0087;
0; Mismatches 157;
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                                                                                                                                                                                                                           157;
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Best Local Similarity
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                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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      168
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IITLE OF INVENTION: A No. 5883226el Human Dopamine Receptor and Uses
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ER OF SEQUENCES:
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5883226
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300 South Wacker Drive
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1508..1610
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SYSTEM: PC-DOS/MS-DOS
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                                                  Score 49.8; DB Pred. No. 0.01; 0; Mismatches
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PCT-US93-07370-12
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME/KEY:
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                                       FEATURE:
                                                                                                                              OTHER INFORMATION:
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                                                                                                                                                                LOCATION: 346..682
IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature LOCATION: 257..262
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/evidence=EXPERIMENTAL

/standard_name= "Alternate Exon 3: D4.7"

/note= "This sequence represents the third exon
allele D4.7 of the human D4 dopamine receptor
                                                                                                                                                                                                                                     /label= PstI
/note= "This sequence is a PstI site whereby
digestion of human genomic DNA produces a RFLP"
                                                                                                                                                                                                                                                                                                                                                                                                                        gene"
                                                       /note= "This sequence is a repeat found in 7 known alleles of the human D4 dopamine receptor gene encoding a 16 amino acid sequence repeated 7 times
                                                                                                    /rpt_type= "tandem"
/evidence= EXPERIMENTAL
/rpt_unit= 346 . 394
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                                                                                                                                                                                                                                                                                                                              ): experimental
/function= "PstI site"
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                                                                                                                                               experimental t_type= "tandem"
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Matches 144;

Conservative

0

Mismatches

157;

Indels

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                                                            PCT-US93-07370-21
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Best Local Similarity
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21, Application PC/TUS9307370
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PINFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 2: COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                        FEATURE:
                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: A Novel Human Dopamine
                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                            MOLECULE TYPE: . cDNA
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                                                                        NAME/KEY:
LOCATION:
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                                                                                                                      LOCATION:
                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                      TYPE: nucleic acid
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                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                            FOPOLOGY:
                                                                                                                                                                 OCATION:
                                                                                                                                                                                                                                                                       ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGCCCCCGCGCCCCGGCCTCCCCCGGACCCCTGCGGCTCCAACTGTGCTCCCCCCGACG
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104..1507
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1508..1610
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Pred. No. 0.0087;
0; Mismatches 157
Score 49.8; DB Pred. No. 0.01;
             DB 5;
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             Length 1610;
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                                                                              Query Match
Best Local Similarity
                                                                 Matches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08623471 Patent No. 5846823
                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 27-SEP-1994
                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: AL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416)-868-1482
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                          cgagettegetgteegegeceagtgaegegegtgeggaeeeegageeeeaatetgeaeee 64
cocacacagotytaatcagococcaggacoccaccettotcatoggotoctcotcctgcaag 304
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                                                                                                                                                                                     nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mississauga
                                                                                                                                                                                                                                                                                                                 RIDOUT & MAYBEE, Attn. Robert G. Hirons NCE/DOCKET NUMBER: ALLEL/51B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6850 Goreway Drive
                                                                 Conservative
                                                                                                                                                                                                                                                                        (416)-362-0823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Owolabi, Joshua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.25
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                                                                                                                                                            linear
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                                                                                                                                                                                                                                        80
                                                                           Score 49.2; DB 4;
Pred. No. 0.0095;
                                                            Mismatches
                                                            153;
                                                                                           Length 345;
                                                            Indels
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                                      Matches
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Best Local (
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                                                                                                                                                                                                                                               TELEFAX: (212) 391-0525 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tent No.
                                                                                                                                          HYPOTHETICAL:
                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                          TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                         NAME: White, John P. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : New York
                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10036
                                                                                                                                                                                                   nucleic acid
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5849564
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1185 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Russo, James J
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                                                                                                                                                                                                                                                                                                                                   John P.
                                                                                                                                                        DNA (genomic)
                                                                                                                                                                                     single
                                                  2.7%;
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                                                                                                                                                                                                                                                16:
                                Score 44.6; DB 4;
Pred. No. 0.12;
0; Mismatches 84
                                                                                                                                                                                                                                                                                                           52342
                                   84;
                                                             Length 801;
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                                Gaps
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GCCCCGGGGCCTGCGCCGCCGCGGGGGCGGGGGCCCTCGCGCTCCGCTGCCGCG 181

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US-07-669-171-3
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                                                     US-08-267-803B-8
          Sequence 8, Application US/08267803B Patent No. 5834183 GENERAL INFORMATION:
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                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 66141 PENNIE
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                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
-669-171-3
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LENGTH: 1569 base pairs
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 18,872 REFERENCE/DOCKET NUMBER: 56
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LE OF INVENTION:
BER OF SEQUENCES:
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SYSTEM: PC-DOS/MS-DOS
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Pred. No.
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GENERAL INFORMATION:

Application US/07669171

APPLICANT:

ANTHONY F

PPLICANT:

ITLE OF INVENTION:

TGF-b1/b2: A NOVEL CHIMERIC TRANSFORMING GROWTH FACTOR-BETA

MERWIN, JUNE RAE

OF SEQUENCES:

& EDMONDS

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; NAME/KEY:
; LOCATION:
US-08-267-803B-8
                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 80; Conserv
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INFORMATION FOR SEQ ID NO:
10618 AAAAAAAAAAAAAAAAAAA 10637
                                                                                                                         10498 TTTGATTCAAAATTTGAACAAAATTGTTTTAAATAAATTGTCTGTATACCAGTACAAGTT 10557
                                                            1610 aaaaaaaaaaaaaaaaaaa 1629
                                                                                                                                                 1490 tttggtccacatgatggtcacacttggatataccccagtgtgggtaaggttggggtattg 1549
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NAME: McCormack, Myra H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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LECOMMUNICATION INFORMATION:
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P.O. Box 581415
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STREET: 1155 AVENUE OF THE AMERICAS
CITYY: NEW YORK
STATE: N.Y.
COUNTRY: U.S.A.
2 IP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/07/669,171
FILING DATE: 19910314
CLASSIFICATION: 435
APTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-159-999
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-790-9090
TELEFAX: 66141 PENNIE
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1560 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
'COTECUTE TYPEF: DNA (genomic)
Search completed: September 28, 1999, 16:39:08 Job time: 6934 sec
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LOCATION: 261..1430
S-07-669-171-1
                                                                                                                                                                                                                                                                                                                                 Query Match 2.7%; Score 43.6; DB 1; Length 1560; Best Local Similarity 63.2%; Pred: No. 0.23; Matches 67; Conservative 0; Mismatches 39; Indels 0;
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1731 1732

T61348 T61332

Batten disease Batten disease

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Database
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1629
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                       segs,
                      125096042 residues
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(without alignments)
1341.506 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. a a 1563 1532 1339 966 961 932 932 799 452 Score Query Match 100.0 94.1 82.2 82.0 59.3 59.3 59.3 59.3 Length 멂 T13229 V143613 T61336 T61336 T61336 T61336 T61338 T61338 T61340 T61342 T61342 T61344 T61344 T61344 T61344 T61344 V09036 V09039 Q57657 T27547 V27140 V27141 V41688 V70896 V27158 N90929 X53491 Ħ SUMMARIES Human secreted pro Batten disease gen HSV L/ST region. H Infected cell prot The nucleotide seq Human adenosine Al Equine arteritis v Equine arteritis v Allele D4.7 of the Recombinant human Non-overlapping re Polydeoxyribonucle OR-1 orphan recept Expressed sequence Expressed sequence HSV L/ST region. H Human dopamine D4. Nucleotide sequenc Nucleotide sequenc Nucleotide sequenc cDNA encoding an a Unspliced murine N Nucleotide sequenc cDNA encod cDNA encoding Nucleotide sequenc Novel haemopoietin Novel haemopoietir Description haemopoietin

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CTGTCCTCGCTGTCGCCTCTGTTGCTCTGTGTCCTCGGGGTGCCTCGGGGGCGGATCG cccatgcccgcgggtcgcccggtcgcccaatccgcgcggcggccgcgcggcggccg

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180 120 120 60 60 Query Match
Best Local Similarity
Matches 1629; Conserv

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Score 1629; Pred. No. 0; Mismatches

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Length 1629; Indels

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RESULT
V27140
Claim 4; Page 77-81; 182pp; English.

The haemopoletin receptor (HR) NR6.1 is a form of the novel HR NR6. Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening. Sequence 1629 BP; 336 A; 541 C; 453 G; 299 T;
                                                                                                                                                                                New isolated haemopoletin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells
Claim 4; Page 77-81; 182pp; English.
                                                                                                                                                                                                                                                                                19-MAK-1970.
11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS PTY LTD.
(DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Alexander W, Fabri L, Farley A, Hilton Rakar S, Willson
                                                                                                                                                                                                                                                           WPI; 98-260970/23.
P-PSDB; W55011.
                                                                                                                                                                                                                                                                                                                                                                                                                     WO9811225-A2.
19-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel haemopoletin receptor NR6.1 gene. Haemopoletin receptor; cell proliferation; cell survival; therapeutic; neuronal proliferation;
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113. .1355
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ctgctgggtcagacctggaggctcacctgaattggagcccctctgtaccatctgggcaac
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11-SEP-1997; G02479.

11-SEP-1996; AU-002246.

11-SEP-1996; AU-002246.

(AMRA-) AMRAD OPERATIONS PTY
(DZIEZ) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley
Kojima T, Maeda M, Nash A, N
                                                                                                                  The haemopoletin receptor (HR) NR6.2 is a form of the novel HR NR6. Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening. sequence 1673 BP; 344 A; 550 C; 474 G; 305 T;
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CDS
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Novel haemopoietin receptor NR6.2 gene.
Haemopoietin receptor; cell proliferation; cell different
cell survival; therapeutic; neuronal proliferation; drug
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New isolated haemopoletin receptor - used for for modulating proliferation, differentiation e.g. neuronal cells
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Nicola NA, F
Score 1563.4;
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                CCGCGTGGAGGACAGCGTGGAAGGTGGTGGATGACGTCAGCAACCAGACCTCCTG
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PT New nucleic acid encoding U4 haematopoletin receptor superfamily PT chain - potentially useful, e.g. for modulating cell proliferation PT or immune response, for treating cancer and auto: immune disease PS Claim 1; Pages 25-26; 38pp; English.

CC This is the nucleotide sequence encoding the murine U4 protein from CC the haematopoletin receptor superfamily, used in the method of the CC invention for the modulation of cell proliferation, or the immune CC response. Transformed mammalian cells are used to produce recombinant CC U4 protein. The U4 protein is used to screen for specific binding CC agents, raise antibodies. It is also used as reagents for assays and CC at issue markers for isolation of cognate ligands and receptors, and CC in pharmaceutical compositions which may modulate cell proliferation, cell differentiation, and the immune system (e.g. for treating immune CC deficiency, inherited or the result of infection, autoimmune diseases, Sequence 1656 BP; 318 A; 552 C; 478 G; 308 T;
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15-JAN-1999; UO0334.
16-JAN-1999; US-784863.
(GEMY ) GENETICS INST INC.
COllins M, Donaldson DD, N
WPI; 98-414109/35.
P-PSDB; W59804.
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Key
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Nucleotide sequence of the murine U4 gene.
Murine; U4 protein; haematopoietin receptor superfamily;
cell proliferation; immune response; antibody; cell diff
autoimmune disease; cancer; allergy; ds.
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Query Match Best Local

Similarity

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Best Local Similarity 90.6
Matches 1520; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-l on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-l in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and therapeutically to modify Zcytor5 ligand effects.

Sequence 1724 BP; 350 A; 550 C; 500 G; 324 T;
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Pred. No. 1.3e-268;
0; Mismatches 93;
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29-SEP-1998 (first e rine NR6

Unspliced murine Haemopoietin rece cell survival; th (first entry)
rine NR6 nucleotide sequence.
receptor; cell proliferation;
l; therapeutic; neuronal prolif proliferation;

cell differentiation; drug

screening;

Mouse

W0981125-A2.
19-MAR-1998.
11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
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Zhang J;
WPI; 98-260970/;
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NR6 is a novel haemopoletin receptor (HR). Interaction between the nove HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues i vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and disgnosis, e.g. for cancers or predisposition to cancers, or for drug screening.

Sequence 1930 BP; 375 A; 623 C; 561 G; 371 T;
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Nash A, Nicola
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r S, Willson
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V70894
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05-NOV-1998
01-MAY-1998; U08865.
13-FEB-1998; US-074721.
01-MAY-1997; US-045287.
01-MAY-1997; US-850030.
13-FEB-1998; US-023890.
(ZYMO) ZYMOGENETICS INC.
Adams RL, FOSTET DC, Gilbert T
Lok S, Presnell SR, Whitmore T
WFF; 99-034662/03.
P-PSDB; W70860.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA encoding human Zcytor5.
Zcytor5; cytokinin-like receptor;
maintenance factor; thyroid; hear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V70894;
down-regulating
in blood
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                         cytokinin-like receptor Zcytor5 - useful for,
ng Zcytor5 natural ligands or detecting cardio
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enlargement; Zcytor!
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t; skeletal muscle; cardiotrophin-1;
nent; Zcytor5 ligand; ss.
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                         cardiotrophin-1
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79 The present sequence encodes a protein designated Zcytor5, which is converted to the present sequence of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart cenlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcytor5 and therapeutically to modify Zcytor5 ligand effects.

79 Sequence 1690 BP; 319 A; 592 C; 505 G; 274 T;
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Best Local Similarity
Matches 1090; Conser
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                                                                                    990cctcttcactccctatgagatctgggtggaagccaccaatcgcctaggctcagcaag
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Pred. No. 1.5e-191;
0; Mismatches 174;
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in blood

Disclosure; Page 68-70; 55pp; English.

The present sequence encodes an allelic varaint of protein designated Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so proventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the enlargement and to discover other possible Zcytor5 ligands. A probe
                                                                                                                                                                                                                                            WO9849307-A1.
05-NOV-1998.
01-MAY-1998; U08865.
13-FEB-1998; US-074721.
01-MAY-1997; US-045287.
01-MAY-1997; US-850030.
13-FEB-1998; US-023890.
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
Key
CDS
                                                                                                                                                                                                                                                                                                                                                                                                                       17-MAR-1999 (first entry)

DNA encoding an allelic varaint of human Zcytor5.

Zcytor5; cytokinin-like receptor; down-regulation; growth factor;

maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;

cardiac pathology; heart enlargement; Zcytor5 ligand; allelic varaint
                                                                                                                                                                            (ZYMO) ZYMOGENETICS INC.
Adams Rt, Foster DC, Gilbert
Lok S, Presnell SR, Whitmore
WPI; 99-034662/03.
P-PSDB; W70861.
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                                                                                                                                                New mammalian cytokinin-like down-regulating Zcytor5 natur
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                                                                                                                                              -like receptor Zcytor5 - useful for, e.g.
natural ligands or detecting cardiotrophin-1
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Best Local Similarity 84.7%;
Matches 1095; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and anti-idiotypic antibody could be used to purify Zcytor5 and therapeutically to modify Zcytor5 ligand effects.

Sequence 1813 BP: 415 A; 604 C; 519 G; 275 T;
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cgcgtggaggacagcgtggactggaaggtggtggatgacgtcagcaaccagacctcctgc
                             tgggtctcaccagctctcaaggatttcctcttccaagccaagtaccagatccgctac
                                                                        CCCCCGCCCGACGTGCACGTGAGCCGCGTCGGGGGCCTGGAGGACCAGCTGAGCGTGCGC
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Pred. No. 1.8e-190;
0; Mismatches 186;
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Query Match Best Local Sin Matches 1023;

Similarity

57.2%; 87.1%;

Conservative

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Score 932.4; DB Pred. No. 1.8e-11 0; Mismatches 1:

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16-JAN-1997; US-784863.
(GEMY) GENETICS INST IN
Collins M, Donaldson DD,
WPI; 98-414109/35.
Claim 1; Page 28; 38pp; English.

This is the nucleotide sequence encoding the human U4 protein from the haematopoietin receptor superfamily, used in the method of the invention for the modulation of cell proliferation, or the immune response. Transformed mammalian cells are used to produce recombinant U4 protein. The U4 protein is used to screen for specific binding agents, raise antibodies. It is also used as reagents for assays and at issue markers for isolation of cognate ligands and receptors, and in pharmaceutical compositions which may modulate cell proliferation, cell differentiation, and the immune system (e.g. for treating immune deficiency, inherited or the result of infection, autoimmune diseases, cancer, and allergy).

Sequence 1579 BP; 304 A; 535 C; 473 G; 267 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUL-1998.
15-JAN-1998;
16-JAN-1997;
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Key
CDS
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Nucleotide sequence of the human U4
Human; U4 protein; haematopoietin re
cell proliferation; immune response;
autoimmune disease; cancer; allergy;
                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding U4 haematopoietin receptor superfamily chain - potentially useful, e.g. for modulating cell proliferation or immune response, for treating cancer and auto:immune disease
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19-MAR-1998.

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(AMRA-) AMRAD OPERATIONS PTY LT

(DZIE/) DZIEGLEWSKA H E.

(DZIE/) DZIEGLEWSKA L, Failey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The nucleotide sequence was generated by a 5N RACE of brain cDNA using NR6 specific primers. NR6 is a novel Haemopoletin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening. Sequence 834 BP; 167 A; 274 C; 225 G; 168 T;
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29-SEP-1998 (first entry)
Nucleotide sequence of products generated by 5N race
Haemopoietin receptor; cell proliferation; cell diff
cell survival; therapeutic; neuronal proliferation;
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WPI; 98-260970/23.
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Nicola NA, Rakar S, Willson
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W09811225-A2.

19-MAR-1998.

2 19-MAR-1998.

F 11-SEP-1997; G02479.

PR 11-SEP-1996; AU-002246.

PA (AMRA-) AMRAD OPERATIONS PTY LTD.

PA (DZIE/) DZIEGLEWSKA H E.

PA (DZIE/) MARAD OPERATIONS PTY LTD.

Alexander W, Fabri L, Farley A, Hilton DJ

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Nucleotide sequence of clone
Haemopoletin receptor; cell p
cell survival; therapeutic; n
New isolated haemopoletin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells (laim 7; Page 102-104; 182pp; English. The NR6 gene encodes a novel Haemopoletin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation. The HR and it's differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of differenticells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and diagnosis, and survival. The products can also be used for detection and diagnosis,
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                      cacgcatactgctcgaaccttagtttccgcctgtacgaccagtggcgtgcttggatgcag
                                                    cgcgtggaggacagcgtggactggaaggtggtggatgacgtcagcaaccagacctcctgc
                                                                                                                                                                                               tgggtetcaccaccagetetcaaggatttcetettecaagccaagtaccagatecgetac
                                                                                                                                                                                                                             cccccaccgacgtgcacgtgagccgcgttgggggcctggaggaccagctgagtgtgcgc
                                                                                                                                                                                                                                                          ATCCCCAAGGACCTGGCTCTCTTTACGCCCTATGAGATCTGGGTGGAGGCCACCAACCGC
                                                                                                                                                                                                                                                                                                atccccaaggacctggccctcttcactccctatgagatctggggtggaagccaccaatcgc
                                                                                                                                                                                                                                                                                                                      TGGTATGGCCAGGACAACACATGTGAGGAGTACCACACAGTGGGGCCCCACTCCTGCCAC
                                                                                                                                                                                                                                                                                                                              CCAGGGGCCCACGGGGAGACCTTCCTCCACACCAACTACTCCCTCAAGTACAAGCTTAGG
                                                                                                                                                                                                                                                                                                                                                            ANACCCGTCANCATCAGCTGCTGGTCCAAGAACATGAAGGACTTGACCTGCCGCTGGACG
                                                                                                                                                                                                                                                                                                                                                                                         aagccctttaacatcagctgctggtcccggaacatgaaggatctcacgtgccgctggaca
aagtcacacaagacccgaaaccaggtcctgccg
                                            CACGCGTACTGCTCCAACCTCAGCTTCCGCCTCTACGACCAGTGGCGAGCCTGGATGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 799.4; I
Pred. No. 5.6e
0; Mismatches
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6.6e-157;
es 121;
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Best Local Similarity
Matches 493; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NR6 is a novel haemopoletin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.

Sequence 560 BP; 113 A; 182 C; 165 G; 100 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS PTY LTD.
(DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
KOjima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 101; 182pp;
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PCR product for human NR6.
Haemopoletin receptor; cell proliferation; cell differentiation; car cell survival; therapeutic; neuronal proliferation; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated haemopoietin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCTATGAGATCTGGGTGGAGGCCACCAACCGCCTGGGCTCTGCCCGCTCCGATGTACTC
                                                                                                                                                                                                                                                                                                                      gagtaccactgtgggccctcactcatgccatatccccaaggacctggccctcttcact
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g.ttgggggcctggaggaccagctgagtgtgcgctgggtctcaccaccagctctcaaggat
                                                                                      acactggatgtcctggacgtggtgaccacggacccccaccgacgtgcacgtgagccgc
                                                                                                                                                                                                                                                                                  GAGTACCACACAGTGGGGCCCCACTCCTGCCACATCCCCAAGGACCTGGCTCTTTTACG
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Pred. No. 2.3e-85;
0; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  developing products and survival of cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 560;
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19-MAR-1998.

F 11-SEP-1997; G02479.

R 11-SEP-1996; AU-002246.

A (AMRA-) AMRAD OPERATIONS PTY LTD.

PA (DZIE/) DZIEGLEWSKA H E.

PA (DZIE/) DZIEGLEWSKA H E.

PA "1-vander W, fabri L, Farley A, Hilton DJ
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                                                                                                                                                                                          Query Match
Best Local S
Matches 305
                                                                                                                                                                                                                                                        The haemopoletin receptor (HR) NR6.3 is a form of the novel HR NR6. Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, sequence one one predisposition to cancers. Or for Arma Sequence one one predisposition to cancers.
                       1222
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                                                                                                                   1102
                                                                                                                                                                                                                                                                                                                                                                       for modulating proliferation,
e.g. neuronal cells
e.g. neuronal cells
Claim 6; Page 90-92; 182pp; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel haemopoletin receptor NR6.3 gene. Haemopoletin receptor; cell proliferation; cell survival; therapeutic; neuronal proli
                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; W55013.
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29-SEP-1998 (first entry)
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181
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                                          cggcgcgagctcaagcagttcctcggctggctcaagaagcacgcatactgctcgaacctt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                        Similarity 100.
05; Conservative
                                                                                                                                                                                                                                                      938
                                                                                                                                                                                                                                                      BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                  predisposition to cancers, 243 A; 245 C; 272
                                                                                                                                                                                                    18.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              938
                                                                                                                                                                                                                                                                                                                                                                                                receptor - used for ion, differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Haemopoietin receptor
                                                                                                                                                                                        %; Score 305; DB
%; Pred. No. 9.5
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rakar
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DJ, Kikuchi
Rakar S, Wil
                                                                                                                                                                                                                DB 1;
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s 0;
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feration; drug screeni;
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                                                                                                                                                                                                                                                                                                                                                                                                developing products and survival of cel
                                                                                                                                                                                                              Length 938
                                                                                                                                                                                                                                                 for drug screening.
178 T;
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                                                                                                                                                                                      Gaps
                                            180
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19-MAR-1998.
11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
1 (AMRA-) AMRAD OPERATIONS PTY LTD.
A (DZIE/) DZIEGLEWSKA H E.
A (DZIE/) DZIEGLEWSKA H E.
Yowander W, Fabri L, Farley A, Hilton DJ
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                               Matches
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The NR6 protein is a novel Haemopoletin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnossis, e.g. for cancers or predisposition to cancers, or for drug screening.

Sequence 11832 BP; 2447 A; 3367 C; 3298 G; 2720 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tor modulating proliferation, e.g. neuronal cells
Claim 9; Fig 3: 182pp. car?''
                                                                                                                                                6450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence for muri
Haemopoietin receptor; cell
cell survival; therapeutic;
                                        6570
                                                                                            6510
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W09811225-A2.
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14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isolated haemopoletin receptor - used for developing products modulating proliferation, differentiation and survival of cells,
                                                                                                                                                                                              cctgctctatacatggagacacacctggggccaccgctgaggggctctactggaccctca
                                                                                                                                                                                                                                                                   acacagetgtaatcagececeaggaceceacetteteateggeteetecetgeatgcta
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                                    atggtcgccgcctgccctctgagctgtcccgcctccttaacaccctccaccctggccctgg
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                                                                                        ccctggctaaccttaatgggtccaggcagtcaggagacaatctggtgtgtcacgccc
                                                                                                                                            ATGGTCGCCGCCTCTGAGCTGTCCCGCCTCCTTAACACCTCCACCCTGGCCCTGG
                                                                                                                                                                                                                                                       ACACAGCTGTAATCAGCCCCCAGGACCCCACCCTTCTCATCGGCTCCTCCCTGCAAGCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGTTTCCGCCTGTACGACCAGTGGCGTGCTTGGATGCAGAAGTCACACAAGACCCGAAAC
                                                                                                                                                                                                                                                                                                             281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                        17.2%;
99.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               murine NR6 containing additional 5N sequencell proliferation; cell differentiation; tic; neuronal proliferation; drug screening
                                                                                                                                                                                                                                                                                                         Score 280.4;
Pred. No. 1.9e
0; Mismatches
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Rakar S, Willson
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                                                                                                                                                                                                                                                                                                          1;
                                     6611
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ij

V27145

standard;

DNA;

6663

ВP

Expressed sequence tag used to identify human zcytor5. Zcytor5; cytokinin-like receptor; down-regulation; growth factor; maintenance factor; thyroid; heart; skeletal muscle; cardiotrophi

ligand;

cardiotrophin-1;

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19-MAR-1998
11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS PTY L
(DZIE/) DZIEGLEWSKA H E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            The NR6 gene encodes a novel Haemopoietin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's products can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening. Sequence 6663 BP; 1462 A; 1852 C; 1715 G; 1634 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated haemopoletin reco
for modulating proliferation,
e.g. neuronal cells
Claim 8; Page 108-114; 182pp;
The NR6 gene encodes a novel 1
                                                V70897;
17-MAR-1999
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WPI; 9
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02-OCT-1998
                                                                         V70897
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Haemopoletin receptor; cell proliferation; cell differentiation; cancer; cell survival; therapeutic; neuronal proliferation; drug
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P-PSDB; W55016.
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Nash
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Wash A, Nicola NA, R/
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99.6%;
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Pred. No. 1.7e-49;
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Rakar S, Willson
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Best Local Similarity 81.3%;
Matches 209; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents an expressed sequence tag (EST) used to identify cDNA encoding a protein designated Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-l on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-l in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodyes antibody could be used to purify Zcytor5 and the therapeutically to modify Zcytor5 ligand effects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1998; U08865.
13-FEB-1998; US-074721.
01-MAY-1997; US-045287.
01-MAY-1997; US-045287.
13-FEB-1998; US-023890.
                        1163 cgggcccgggcggcggg 1179
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Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
Lok S, Presnell SR, Whitmore TE;
                                                                                                                                                                                         120
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NGGGCCCGGGNGGNGGG 256
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Pred. No. 9.4e-29;
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Search completed: September 28, 1999, 16:44:42 Job time: 7267 sec

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SUMMARIES

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ALIGNMENTS

ACCESSION NID	RESULT 1 AA049280 LOCUS DEFINITION
CLONE IMAGE: 479043 5' SIMILAT tO SW:IL6B_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR ;, mRNA sequence. AA049280 g1755311	AA049280 464 bp mRNA EST 30-DEC-1996 mj45d02.rl soares mouse embryo NbMEl3.5 14.5 Mus musculus cDNA

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JOURNAL COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:289787
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Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1996)
On Dec 30, 1996 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
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100.0%; Pr
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                                                                                                                                                                                                                       Score 464;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W66776 482 bp mRNA EST 14.JUN-1996 mel7bl1.rl Soares mouse embryo.NbME13.5 14.5 Mus muscullus cDNA clone IMAGE:387741 5' similar to PIR:B3852 B38252 granulocyte colony-stimulating factor receptor precursor; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 482)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub Geisel,S., Kucaba,T., Lacy,M., Le;M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B. Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W6677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1996)
On Apr 14, 1993 th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston, R.
The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                             Possible reversed clone: similarity
                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                              primer: ETPrimer
                                                                                                                                                                                                                                                          quality sequence stop:
Location/Qualifiers
           /tlssue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                               /clone_lib="Soares
/sex="unknown"
                                                                                                                                                                             /db_xref="taxon:10090"
/map="10 pter-cen"
                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                            /clone="IMAGE:387741"
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                                                                                                                                             mouse
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                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 428)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
                                                                                                                                                                                                                                         complete sequence [Homo AA866388
                                                                    Genome Res. 6 (9),
                                                                                              Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two appr
 Contact: Soares,
Program for Rat
                                                                                                                                                                      Rattus norvegicus
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                                                                                                                                                                                                               GI:4230568
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Discovery
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JOURNAL MEDLINE COMMENT

16,

Mapping

discovery

REFERENCE AUTHORS TITLE

KEYWORDS. SOURCE ORGANISM

Norway rat.

ACCESSION NID

ERSION

ÃA866388.1

RESULT AAB66388

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DEFINITION

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Matches 470; Conserv

Query Match Best Local

BASE COUNT ORIGIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTGGGTCTCACCACCAGCTCTCAAGGATTTCCTCTTCCAAGCCAAATACCAGATTCGCT
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Teax: 319 335 9565

Email: msoars@blue.weeg.ulowa.edu

Coligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics
  AI421423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: M13 Forward
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451 Eckstein Medic
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/note-"Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; This library consists of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, and muscle. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="sprague-Dawley"
/db_xref="taxon:10116"
/db_xref="taxon:10116"
/map="between D11S1765 and UGB"
/clone="UI-R-A0-aj-f-04-0-UI"
/clone_11b="UI-R-A0"
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/strain="Sprague-Dawley"
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                                                                      tatacatggagacacacctgggggccaccgctgaggggctctactgggaccctcaatggtcg 374
                                                                                                                    TGTGATCAGTCCCCAGGATCCCACGCTTCTCATCGGCTCCTCCCTGCTGGCCACCTGCTC 120
                                                                                                                                           tytaatcayccccaygaccccaccettctcatcygctcctccctycaayctacctyctc 314
ccgcctgccctctgagctgtcccgcctccttaacacctccaccctggccctggccctggc 434
                                           AGTGCACGGAGACCCACCAGGAGCCACCGCCGAGGGCCTCTACTGGACCCTCAATGGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 474)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insert Length: 1664 Std Err
Seq primer: -40UP from Gibco
High quality sequence stop: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: David N. Louis, M.D., Myrna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tf25h01.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2097265 3/similar to SW:IL6B_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apr 7, 1998 this sequence version replaced gi:3034955
                                                                                                                                                                                                                                                                                                                                                                                                           81
                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adaptors (Pharmacia), digested with Not I the Not I and Eco RI sites of the modified Library is normalized, and was constructed Soares and M.Fatima Bonaldo."

181 c 128 g 83 t 1 others
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//clone_lib="NCI_CGAP_Brn23"
//tissue_type="911oblastoma (pooled)"
/lab_host="DH10B"
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
On Feb 17, 1998 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 467.
                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1552 Std Error: 0.00 Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov
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fetal heart NbHH19W.
183 c 129 g
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/clone_lib="Soares_fetal_lung_NbHL19W"
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Query Match
Best Local Similarity
Matches 403; Conserv

Conservative

22.3%; 85.6%;

Score 362.8; DB 43; Pred. No. 2.3e-60; Mismatches

Length

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WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep.
4444 Forest Park Parkway, Box 8501, St. Lc
Tel: 314 286 1800
                                                                                                                                                                                                        The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Dec 30, 1996 this sequence version
                                                                                                                                                                                                                                                               Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque, Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood;K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                          This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Eutheria; Rodentia;
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mj45c04.rl Soares mouse
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primer: -28M13 rev2 from Amersham
h quality sequence stop: 486.
Location/Qualifiers
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314 286 1810
                                                                                          mouseest@watson.wust1.edu
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5', mRNA sequence.
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further information
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                    AI394468 462 bp mRNA
tf79d12.x1 NCI_CGAP_Brn23 Hor
mRNA sequence
AI394468
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14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2]; double-stranded cDNA was ligated Eco RI adaptors (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"Vector: pT7T3D-Pac (Pharmacia) with a modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:479046"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="13.5-14.5dpc
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="unknown"
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Pred. No. 3.6e
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                                                                                                                                                                                                                       1 GCCCCTGCTGCTGCTCTCGGGGCGCGCGGGGGCGGGATCAGGAGCCCACACAGC
                   ccgcctgccctctgagctgtcccgcctccttaacacctccaccctggccctggccctggc 434
                                                                                         tatacatggagacacacctgggggccaccgctgaggggctctactggaccctcaatggtcg 374
 CCGCCTGCCCCTGAGCTCTCCCGTGTACTCAACGCCTCCACCTTGGCTCTGGCCCTGGC
                                                                                                                                               TGTGATCAGTCCCCAGGATCCCACGCTTCTCATCGGCTCCTCCCTGCTGGCCACCTGCTC
                                                                       AGTGCACGGAGACCCACC
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1. (bases 1 to 462)

NCININDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /ww-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                  Similarity
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                         adaptors (Pharmacia), digested with Not I the Not I and Eco RI sites of the modified Library is normalized, and was constructed Soares and M.Fatima Bonaldo."

181 c 122 g 79 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="10; 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE: 2105495"
/clone_11b="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
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Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
IMAGE through the consortium info@image.llnl.gov)
Insert Length: 1599 Std Error: 0.00
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High quality sequence stop: 454.
Location/Qualifiers '
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Eutheria; Primates;
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                                                                                                                                      /dev_stage="19 weeks"
//lab_host="DBHOB (ampicillin resistant)"
//lab_host="DBHOB (ampicillin resistant)
//lab_hos
                                  same fetus as the fetal lung NbHL19W."
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/db_xxef="taxon:9606"
/map-"839602; 821611; 4; 4p15.33-4p16.1;
/clone="IMAGE:1705398"
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r Institute, Cancer Genome Anatomy Project (CGAP),
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Query Match Best Local

Similarity

21.7%; 85.6%;

Score Pred.

354; No. 1

DB 43;

Length 466

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REFERENCE
AUTHORS
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qe44h04.x1 Soa:

'IMAGE:1741879

AI185780
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Email: Robert C
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                                                                                                                                                                                                            Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL;
                                                                                                                                                                                                                                                                                                             Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                     IMAGE Consortium (info@image.llnl.gov)
Insert Length: 1622 Std Error: 0.00
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National Cancer Institute, Cancer Genome Anatomy
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Eutheria; Primates; Catarrhini;
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h quality sequence stop: 466.
Location/Qualifiers
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/lab_host="DH10B (ampicillin resistant)"
/note="Organ: lung; Vector: pT7T3D (Pharmacia) with
modified polylinker; Site_1: Not I; Site_2: Eco RI;
                                                /clone="IMAGE:1741879"
/clone_lib="Soares_fetal_lung_NbHL19W"
/dev_stage="19 weeks"
                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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Soares_fetal_lung_NbHL19W
.879 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  normalization to a Cot - 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbHH19W."

183 C 123 g 80 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             double stranded cDNA was size selected, ligated to Eco adapters (Pharmacia), digested with Not I and cloned i the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 354; DB 43;
Pred. No. 1.1e-58;
0; Mismatches 66;
   465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ed to Eco RI
cloned into
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                                                                                                                                366
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REFERENCE
AUTHORS
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ORGANISM
                                                                                                                                                                                                                                             VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 445)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
The WashU-HHMI Mouse EST Project 
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                           m199d07
                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                  AA039053.1
                                                                                                                                                                                                                          house mouse
                                                                                                                                                                                                                                                                                                                  053 445 bp mRNA
07.rl Soares mouse embryo NbME13.5
IMAGE:474733 5', mRNA sequence.
                                                                                                                                                       Chordata; Craniata; Vertebrata;
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                       EST
14.5
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BASE COUNT
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Best Local S
Matches 395
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                                                                                                                          1463
                                                                                                                                                                   1403 tcacctgaattggagcccctctgtaccatctgggcaacaaagaaacctaccagaggctgg 1462
                                                                                                                                                                                                                                                                                             1326 acacaagacccgaaacc-----
                                                                                                                                                                                                                                                                                                                                                    1266
                                                                                                                                                                                                                                                                                                                                                                              445
                                                                                                                                                                                                                                                                   325
                                                                                                                                                                                                            265
                                                                                                                                                                                                                                                                                                                         385 ATACTGCTCGAACCTTAGTTTCCGCCTGTACGACCAGTGGCGTGCTTGGATGCAGAAGTC
                                           85
                                                                                                                                                                                                                           aggtcctgccggctaaactctaaggataggccatcctcctgctggtcagacctggaggc 1402
                                                                                                                                                                                                                                                                                                                                       atactgctcgaaccttagtttccgcctgtacgaccagtggcgtgcttggatgcagaagtc 1325
                                                                                                                                                                                                                                                                                                                                                                              ACACAAGACCCGAAACCAGGACGAGGGGATCCTGCCCTCGGGCAGACGGGGTGCGGCGAG
aggagttgttcaggtaaaaaaaaaa 1607
                                                                                                             ggcacaatgagctcccacaaccacagctttggtccacatgatggtcacactttggatatac
                                                         GGCACAATGAGCTCCCACAACCACAGCTTTGGTCCACATGATGGTCACACTTGGATATAC
                                                                                                                                                       TCACCTGAATTGGAGCCCCTCTGTACCATCTGGGCAACAAAGAAACCTACCAGAGGCTGG
                                                                                                                                                                                                            AGGTCCTGCCGGCTAAACTCTAAGGATAGGCCATCCTCCTGCTGGGTCAGACCTGGAGGC
                                           395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Marra M/Mouse EST Project
washington University School of MedicineP
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI:285477
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:474733"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone_lib-"Soares mouse embryo NbME13.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ი
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 337.8; DB 27; Pred. No. 1.4e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 g
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 t
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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                                                                                                                                                                                                                                                                                                  1343
                                                                                                                                                        146
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                                                                                                                              1522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
TITLE
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AI187074
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BASE COUNT
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Best Local Similarity
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354 ctactggaccctcaatggtcgccgcctgcctctgagctgtcccgcctccttaacacctc
                                                                                                                                                                                                                                                                                                                                                                                                                                                               174
                                                                                                                                                                                 294
                                                                                                                                                ctocotgcaagctacotgctotatacatggagacacacottggggccaccgctgaggggct 353
                                                                                                                                                                                                                                                                                        cggatcgggagcccacacagctgtaatćagcccccaggaccccacccttctcatcggctc
                                                                                                                                                                                                                                                                                                                                                                                                                                     gcggccgctgtcctcgctgtggtcgcctctgttgctctgtgtcctcggggtgcctctgggg 233
                                                                                                              CTCCCTGCTGGCCACCTGCTCAGTGCACGGAGACCCACCAGGAGCCACCGCCGAGGGCCT
                                                                                                                                                                                                                                                       CGGATCAGGAGCCCACACAGCTGTGATCAGTCCCCAGGATCCCACGCTTCTCATCGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                376;
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ge38a03.s1 Soares_fetal_lung_NbHL19W

IMAGE:1741228 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
On Aug 21, 1998 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              National Cancer Institute,
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National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Clone_Iib="Soares_fetal_lung_NbHL19W"
/clone_lib="Soares_fetal_lung_NbHL19W"
/clone_lib="Soares_fetal_lung_NbHL19W"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/lab_host="DH10B (ampicillin resistant)"
/lab_host="PH10B (am
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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/dh yref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 334; DB 43;
Pred. No. 7.4e-55;
0; Mismatches 71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 447;
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FEATURES
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AUTHORS
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KEYWORDS
BASE COUNT
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AI333812
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                                                                                                                                                                                                                                                                                                                  source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  594 ctggacaccgggtgcacacgggggagac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCAGAGAAACCCGTCAACATCAGCTGCTGGTCCAAGAACATGAAGGACTTGACCTGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CACCTTGGCTCTGGCCCAGCCTCAATGGGTCCAGGCAGCGGTCGGGGGACAACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTACTGGACCCTCAACGGGCGCCGCCTGCCCCTGAGCTCTCCCGTGTACTCAACGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGGACGCCAGGGGCCCACGGNGAGAC 447
                                                                                                                                                                                                                                                                                                                                                                                                                 rel: (301) 496-1550
Email: Robert 7
                                                                                                                                                                                                                                                                                                                                                                     AI333812 431 bp mRNA EST 13-FEB-1999 qp93e12.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1930606 3' similar to TR:Q16354 Q16354 PROLACTIN RECEPTOR
                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 407.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                          Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9407037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
AI333812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI333812.1 GI:4070371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 431)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jan 14, 1998 this sequence version replaced gi:1797892
              8
                     /map="4p16.1-4pter"
/clone="IMAGE:1930606"
                                                                                                                                                                                                                   /clone_lib="Soares_fetal_lung_NbHL19W"
/dev_stage="19 weeks"
                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                               organism≈"Homo sapiens"
                                                                                                                                                                                                       lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                  .431
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REFERENCE
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                                                                                          q126b05.xl Soares_NhHMPu_S1
3', mRNA sequence.
A1269388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362;
                                                                                                                                                                      Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                           On Aug 21, 1998 this sequence version
                                                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 417)
                                                                                                                                                                                                                                                                                                                      Homo sapiens
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Similarity 85.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               431
                                                                            quality sequence stop: 406.
Location/Qualifiers
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/tissue_type="Pooled human melanocyte,
               /clone_lib="Soares_NhHMPu_S1"
                           /clone="IMAGE:1857585"
                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 5.6e-53;
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                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                  Anatomy Project (CGAP),
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AUTHORS
                                                           COMMENT
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                                                                                                                                                                                                                                                                  ACCESSION
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Best Local
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7 UI-R-GO-ut-h-08-0-UI.s

UI-R-GO-ut-h-08-0-UI 3

AI579568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351;
Contact: Soares, MB Program for Rat Gene Discovery and Mapping University of Iowa
                                                                                                                                                          Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Ve
Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                1 (bases 1 to 332)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                      Genome Res. 6 (9),
                                                                                                       discovery
                                                                                                                                                                                                          Norway rat.
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                                                            Mar 10,
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                                                            1998 this
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3', mRNA sequence.
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Pred. No. 1.6e-50;
0; Mismatches 66
                                                           sequence version
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ae; Murinae;
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                                                           g1:2948398
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Rattus.
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                                                                                                                                                                                                                                                    gacaatctggtgtgtcacgcccgagacggcag
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                                                                                                                                                                                                                                                                                                                                                                                           GAGGGCCTCTACTGGACCCTCAACGGCCGCCGCCTCAGAGCTGTCCCGTCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                         gaggggctctactggaccctcaatggtcgccgcctgccctctgagctgtcccgcctcctt 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atcggctcctccctgcaagctacctgctctatacatggagacacacctgggggccaccgct 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTCAGGGCGGATCGGGAGCCCACACAGCTGTGATCAGTCCCCAGGACCCCACTCTTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
                                                                                                                                   AI574687 319 bp
UI-R-GO-uc-b-11-0-UI
UI-R-GO-uc-b-11-0-UI
                                                                    EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Research Genetics (www.resgen.com)
Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      451 Eckstein Medical Research
Tel: 319 335 8250
Fax: 319 335 9565
Eukaryota; Métazoa; Chordata; Craniata; Vej
Eutheria; Rodentia; Sciurognathi; Muridae;
                               Norway rat.
Rattus norvegicus
                                                                                   ĀI574687.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B (Life Technologies)"
/note="Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-G0 library is a normalized library constructed from a mixture of rat tissues (nodose ganglia, dorsal root ganglia, and trigeminal ganglia). The tag is a string of nucleotides present between the Not I site and the oligo-dT track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="UI-R-GO-ut-h-08-0-UI"
/clone_lib="UI-R-GO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="Sprague-Dawley
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ∕organism="Rattus norvegicus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dev_stage="adult
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.sl UI-R-GO Rattus
3', mRNA sequence.
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Pred. No. 9.4e-48;
0; Mismatches 23
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                                                                                                                                                    norvegicus
               Vertebrata;
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cDNA clone
 Mammalia;
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Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
Seq primer: M13 Forward.
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Program for Rat Gene Discovery and Mapping
University of Iowa
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Bonaldo, M.F., Lennor
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/note="Vector: pT/T3D-Pac (Pharmacia) with a modified
/note="Vector: pt/T3D-Pac 
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791-806, 1996.
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/clone_lib="UI-R-GO"
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/db_xref="taxon:10116"
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Search completed: September 28, 1999, 15:38:03 Job time: 3271 sec

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1 (bases 1 to 1673)
1 (bases 1 to 1673)
Nicola, N.A., Fabri, L., Farley, A., Nash, A., Willson, T., Rakar, S., Zhang, J., Alexander, W., Hilton, D.J., Kojima, T., Maeda, M. and Kikuchi, Y.
                                                                                 A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME PATENT: WO 9811225-A 19-MAR-1998; NICOLA NICOS ANTONY (AU)
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Zhang, J., Alexander, W., Hilton, D.J., Kojima, T., Maeda, 1
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2 (bases 1 to 1716)
Elson,G.C.A., Graber,P., Lo
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/db_xref="taxon:9606"
/chromosome="19"
/map="19p12"
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/translation="MPAGRRGPAAQSARRPPPLLPLLLLCVLGAPRAGSGAHTAVIS PODPTLLIGSSLLATCSVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALAN LNGSRQASGDNLVCHARDGS ILAGSCLYVGLPEKPVNISCWSKNMKDLTCRWTPGAH GETELHTWSLKYKLRWYGQDNTCEETHTVGHPHSCHLFKLALFTPYEIWVEATUNLG SARSDVLTLDILDVVTTDPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRY RVEDSVDWKVVDDVSNOTSCRLAGLKPGTVFFVQVRCNPFGTYGSKKAGIWSEWSHPT AASTPRSERPGPGGGACEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWR AWJQKSHKTRNQDEGILPSGRRGTARGPAR"
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                                                                                                                       /product="cytokine-like
/protein_id="AAC28335.1"
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/db_xref="GI:3372627"
                                                                                                                                                                                                    /note="similar to cytokine type-1 similar to the sequence presented
                                                                                                                                                                                                                                               /gene="CLF-1"
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Location/Qualifiers
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Nicola, N.A., Fabri, L.,
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Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar, Nicola,N.A., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
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ggctcctgcctctatgttggcttgccccctgagaagccctttaacatcagctgctggtcc 568
                                  tccaggcagcagtcaggagacaatctggtgtgtcacgcccgagacggcagcagtattctggct 508
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Sequence 23
A70393
g4774671
A70393.1 GI
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Location/Qualifiers
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Nicola, N.A., Fabri, L., F
Zhang, J., Alexander, W.,
Kikuchi, Y.
                                                                                                                                                                                                                                                  unidentified unidentified
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                                                                                                                          /organism="unidentified"
/db_xref="taxon:32644"
182 c 165 g 10
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rom Patent
                                                                      Score 452.8; DB 5; Pred. No. 3.2e-85; 0; Mismatches 67;
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Sequence
A70386
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Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., R. Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M.
                                                                                                                                                                                                               A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC Patent: WO 9811225-A 19-MAR-1998; NICOLA NICOS ANTONY (AU)
                                                                                                                                                                                                                                                                                                                                unidentified
                                                                                                                                                                                                                                                                                                                 unclassified
           243
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/db_xref="PID:e4174666"
/db_xref="FID:94174666"
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a 245 c 272 g 178 t
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                                                                                                                                                         /organism-"unidentified"
/db_xref-"taxon:32644"
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Query Match Best Local S Matches 304

h 18.2%; Similarity 100.0%; 04; Conservative (

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Score 304; DB 5; I Pred. No. 3.9e-54; D; Mismatches 0;

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Best Local Similarity 99.6
Matches 281; Conservative
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gagacggcagcattctggctggctcctgcctctatgttggct 530
                     CCCTGGCTAACCTTAATGGGTCCAGGCAGCAGTCAGGAGACAATCTGGTGTGTCACGCCC
                                                                                                                  CCTGCTCTATACATGGAGACACACCTGGGGCCCACCGCTGAGGGGCTCTACTGGACCTTCA 1278
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1 (bases 1 to 6663)

Nicola, N.A., Fabri, L., Farley, A., Nash, A., Willson, T., Rakar, S., Zhang, J., Alexander, W., Hilton, D.J., Kojima, T., Maeda, M. and Kikuchi, Y.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 40668)
Lamerdin,J.E.; McCready,P.M., Adamson,A.W., Burkhart-Schultz,K.,
Gordon,L., Christensen,M., Kyle,A., Ramirez,M., Stilwagen,S.,
Garnes,J., Danganan,L., Bruce,R., Quan,G., Montgomery,M., Ow,D.,
Kobayashi,A., Olsen,A.O. and Carrano,A.V.
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Sequence
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AC003112.1
                                                                                                                                                            sequence,
AC003112
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Human DNA
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A70408.1
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1 (bases 1 to 11832)

1 (bases 1 to 11832)

Nicola, N.A., Fabri, L., Farley, A., Nash, A., Willson, T., Razhang, J., Alexander, W., Hilton, D.J., Kojima, T., Maeda, M.
                                                                                                          human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent: WO 9811225-A 19-MAR-1998;
NICOLA NICOS ANTONY (AU)
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/db_xref="taxon:32644"
3367 c 3298 g 272
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19p12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="predicted exon, program: grail2exons_human_1.3, frame: 1, quality: good, score: 63.000" complement(9529. 9672) /note="predicted exon, program: grail2exons_human_1.3, frame: 1, quality: excellent, score: 75.000" complement(928. .10123) /rpt_family="Nalu" 10409. .10540
                 frame: 1, quality: excellent, score: 100.000--DDS similarity to AA047548 zf15e02.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone 377018 5' (139. 221); 100% identity.--DDS similarity to AA136115 z490b04.rl Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490063 5' (111. 192); 99% identity.--DDS similarity to AA452628 zx33f04.rl Soares total fetus Nb2HF8 9w Homo sapiens cDNA
                                                                                                                                                                                                                                                        /note="DDS similarity to AA047548 zf15e02.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone 377018 5' (1. 138); 96% identity.—other overlapping matches:-(10435. 10548) DDS similarity to AA136115 zk900b4.rl Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490063 5' (1. 110); 93% identity.—-(10466. 10548) DDS similarity to AA452628 zx33f04.rl Soares total fetus Nb2HFB 9w Homo sapiens cDNA clone 788287 5' (1. 82); 95% identity.—-(10486. 10548) DDS similarity to AA009412 ze82h02.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone 365523 5' (1. 61); 97%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="predicted exon, program: grail2exons_human_1.3,
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complement(3269. .3544)
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/db_xref="taxon:9606"
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9254
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_line="5HL2-B"
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NV9 retroviral sequence"
(83. .165); 100% identity .-- DDS similarity
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Incte<sup>®</sup> DDS similarity to AA136115 zk90b04.rl soares pregnant uterus NbHPU Homo sapiens cDNA clone 490063 5' (193. 394); 948 identity.—DDS similarity to AA009412 ze82h02.rl soares fetal heart NbHH19W Homo sapiens cDNA clone 365523 5' (145. 346); 968 identity.—(11121. 1133) DDS similarity to AA009693 ze82h02.sl soares fetal heart NbHH19W Homo sapiens cDNA clone 365523 3' (429. 307); 958 identity.—(11127. 11246) DDS similarity to AA009698 ze82h02.sl soares fetal heart NbHH19W Homo sapiens cDNA clone 365523 3' (429. 307); 958 identity.—(1127. 11246) DDS similarity to AA047548 zf15e02.rl soares fetal heart NbHH19W Homo sapiens cDNA clone 377018 5' (222. 341); 978 identity—(11061. 11331) predicted exon, program: grail2exons_human_l:3, frame: 0, quality: good, score: 73.000--(11061. 11209) DDS similarity to AA452628 zx33f04.rl soares total fetus Nb2HF8 9W Homo sapiens cDNA clone 788287 5' (167. 313); 988 identity."
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pregnant uterus NbHPŪ Homo sapiens cDNA clone 490004 3' (389...343); 99% identity.--DDS similarity to AA127694 zk890:11.r1 Soares pregnant uterus NbHPŪ Homo sapiens cDNA clone 490004 5' (77. ..125); 90% identity.--(15735. .15713) DDS similarity to W46603 zc32h10.r1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 324067.5'
                                                                                                                                                                                                                                                                                                                                        /note="DDS similarity to AA121532 zk89c11.s1 Soares
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/rpt_family="Alu"
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/rpt_family="Alu"
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//note="predicted exon, program: grail2exons_human_1.3,
//note="predicted exon, program: grail2exons_human_1.3,
//note="predicted exon, program: grail2exons_human_1.3,
//note="predicted exon, program: grail2exons_human_1.3,
//note="predicted exons_relation force:
100.000--(18438. .18284) DDS similarity to Whatl31.5 14.5 Mus musculus cDNA clone 387741 5' similar to FIR:B38252 B38252

granulocyte colony-stimulating factor receptor precursor (157. .1); 828 identity --(18438. .18406) DDS similarity to |
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//note="predicted exon, program: grail2exons_human_1.3,
/rame: 0, quality: excellent, score: 81.000-other
overlapping matches:-(15936. .15895) DDS similarity to
AA121532 zk89c11.sl Soares pregnant uterus NbHPU Homo
sapiens cDNA clone 490004 3' (431. .390); 100%
zdientity--(15970. .15895) DDS similarity toAA127694
zk89c11.rl Soares pregnant uterus NbHPU Homo sapiens cDNA
clone 490004 5' (1. .76); 100% identity."
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17926. .18190
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clone Y39B6,
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166494
g2724471
166494.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (09-JUN-1999) Nematode Sequencing Project, Sanger Cent Hinxton, Cambridge CB10 1RQ, UK and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu on Jun 11, 1999 this sequence version replaced gi:4725958. Order of segments is not known; 800 n's separate segments. IMPORTANT: This sequence is unfinished and does not necessarily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may be sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
                                                   Sequence
                                                                   I66494
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/db_xref="taxon:6239"
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                                                                                                                                       Gl gene; glycoprotein; Gs gene; membrane protein; nucleocapsid protein; ORF1a; ORF1a; ORF3; ORF4; replicase; replicase polyprotein; ribosomal frameshift signal. Equine arteritis virus. Equine arteritis virus.
                                                                                                                                                                                                                             g1835169
                                                                                                                                                                                                                                                                PEAVGEN 15528 bp
Plasmid pEAV030 conta
Snijder, E
                                                                                            van
                                                                                                   Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Arteriviridae; Arterivirus.

[ bases 1 to 15528)
                                     point mutation that abolishes Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dorner, F., Scheiflinger, F. and Falkner, F. Gunter. Recombinant fowlpox virus Patent: US 5670367-A 14 23-SEP-1997;
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8; Conser
                                            infections arterivirus cDNA clone: identification of a replicase nt mutation that abolishes discontinuous mRNA transcription
           (bases 1 to 15528)
                                                                                      Dinten, L.C., den Boon, J.A., Wassenaar, A.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1944
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1491 c 1486 g
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2.1%; Pred. No. (
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                                                                                                                                                                                VIAS VIRAIGKPITQESUTATLAALTOODFQFLSDYLDCRAVRSAMNLRAALTSFQVA
QYRNIILNASIQYDRDAARSRRLMAKLADFAVEQEVTAGDRVVVVIDGLDRMAHFKDDLV
                                                                                                                                                                                                                                                                 POATLYMGYWACVAALAVYSLMGLRVKVONVPMCVTPAHFILLARSÄGGSREGMLRVS
AAAPTNSLLGVARDCYVTGTTRLY I FREGELERS PKARGNYGFVAGSSYGTGS
VWTRNNEVVVLTASHVVGRANMATLKIGDAMLTLFFKKNGDDAEAVTTGSELDGNMPO
LHFAOPTIGPÄSMCTATGDEEGLLSGEVCLAWTTSGDSGSAVVGGDAVVGVHTGSNTS
GVAYVTTPSGKLLGADTVTLSCKKHETGPLTS I PKOI PDN LADVDAVPRSLAMLID
GLSKRESSLSGPOLLLIAGEMWSYLNOPAYLPYVLGFFAANFFLPKSYGRPVTGLLM
GCCLFTPLSMRLCLFHLVCATVTGNVISLMFY ITAAGTSYLSEMMFGGYPTMLFVPRF
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                                                                                                                                                                                                                  VTASVTRAYGKPITQESLTATLAALTDDDFQFLSD'
                                  oin(225
                                                                                                                 VPLTTKVVGGSRCTICDVVKEEANDTPVKPMPSRRRRKGLPKGAQLEWDRHQEEKRN
GDDDFAVSNDYVKRVPKYMDPSDTRGTTVKIAGTTYQKVYDYSGNVHYVEHQEDLLD
                                                                                                                                                                                                                                  LYYOFPGWAIGTVLAVCSITMLAAALGHTLLLDVFSASGRFDRTFMMKYFLEGGVKES
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      note="ORF1ab;
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/protein_id="CAA69186
                                                                                    VLGKGSYEGLDQDKVLDLTNMLKVDPTELSSKDKAKARHVAHLLLDLANPVEAVNQL
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/db_xref="taxon:72227"
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/db_xref="taxon:11047"
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'db_xref="taxon:57026"
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'db_xref="taxon:57026"
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frameshift"
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/db_xref="StoTERMBL: 889939"
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/codon_start=1

/db_xref="PID:g1835171" /db_xref="GI:1835171"

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misc_feature
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VTSALAAVSKLIKVPANEPVSFHVASGYRTNALVAPQAKISIGAYAAEWALSTEPPPA
GYAIVRRYIYKRLLSSTEVFLCRRGVVSSTSVQTICALEGCKPLFNFLQIGSVIGPV"
                                                                                                                                                                                                                                                   TRANS LATLON MORESESCYLHWILLICEFESGSILPSAAAWWRGVHEVRVTDLEK DLQCDNLRAKAFESIGYALSIGQSRLSYMLQDWLLAAHRKEVMSNILWSMEGILFDG FDHLDSSYAFFINAYRAALISOYDELQLEAHANKLTHALMILTGE FDHLDSSYAFFINAYRAALISOYDELQLEAHANKLLAVVAFALYHWHLANLTGE TWVPTVGQLHYYASSSIFASSVEVLAAIIILFACIPLVTRVYISFTRLMSPSRRTSS
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VTASVTRAYGKPITQESLTATLAALTDDDFQFLSDVLDCRAVRSAMNLRAALTSFQVA
QYRNILNASLQYDRDAARSRRLMAKLADFAVEQEVTAGDRVVVIDGLDRMAHFKDDLV
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/db_xref="PID:e265651"
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AVVADVGGNIVFGCGPGSHIAVPLQDTLKGVVVNKALKNAAASEYVEGPPGSGKTFHL
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GLSNRESSLSGPQLLLIACFMMSYLNQPAYLPYVLGFFAANFFLPKSVGRPVVTGLLM
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AASFDRWYPHLQALLGFKVDPKKTVNTSSPSFLGCRFKQVDGKCYLASLQDRVTRSLL
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YVLGKGSYEGLDQDKYLDLYNMLKVDPTELSSKDKAKARHVAHLLLDLANPVEAVNQL
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/db_xref="PID:g1835173"
                                                                                                                                                        /note-"ORF3"
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                                                                                                          codon_start=1
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                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 248287)

Bruce, D., Mundt, M., Doggett, N., Munk, C., Saunders, E., Robinso Jones, M., Buckingham, J., Chasteen, L., Thompson, S., Goodwin, L.
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                         Ricke, D.O.
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Bryant,J., Tesmer,J., Meincke,L., Longmire,J., White,S., Tatum
Campbell,C., Fawcett,J., Maltbie,M., Bussod,M., Sutherland,R.,
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FDDMPPFIYYGREFGIVVLDVFMFYPYLVLFFLSVLPYATLILEMCVSILFIIYGIYS
GAYLAMGIFAATLAIHSIVVLRQLLWLCLAWRYRCTLHASFISAEGKVYPVDPGLPVA
AVGNRLLVPGRPTIDYAVAYGSKVNLVRLGAAEVWEP"
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/translation="MGRAYSGPVALLCEFLYECFICGSVGSNNTTICMHTTSDTSVHL
FYAANVTEPSHEQHHFAAAQDEVVHTGYEYAGVTMLVHLFANLVLTFESLVNCSRPVN
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/product="large glycoprotein"
/protein_id="CAA69183.1"
/db_xref="piD:e265652"
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HGHEGCRNFINVTHSAFLYLNPTTPTAPAITHCLLLVLAAKMEHPNATIWLQLQPFGY
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 38 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Qy 403 Db 124032	Qy 343 Db 123972	Qy 283 Db 123912	Oy 223 Db 123852	Qy 163 Db 123792	Qy 103 Db 123732	Qy 43 Db 123672	Query Ma Best Loc Matches	BASE COUNT ORIGIN	FEATURES Sourc						-	
cettaacacetecacetggeeetggeeetggetaace 440 	gtcccgcct 402	totoatoggetcotecetgeaagetacetgetetatacatggagacacacetggggecae 342	ggtgcctcggggggggatcgggagcccacacacagctgtaatcagcccccaggaccccaccct 282	geggeggeegeegeggeegetgteetegetgtggtegeetetgttgetetgttgt	cycccyttycycyccaccccaatycccycygytcycccygygcccyttycyccaatccyc 162	cccgagccccaatctgcacccgcagactcgcccccgccccataccggcgttgcagtcac 102	3.0%; Score 49.8; DB 35; Length 248287; Local Similarity 45.2%; Pred. No. 0.46; hes 180; Conservative 0; Mismatches 218; Indels 0; Gaps	/db_xref="taxon:9606" /clone="480G7" /chromosome="16" 69271 a 54951 c 54455 g 69	* 124504 248287; contig Cocation/Qualifiers e 1.248287 organism="Bomo sant	of 20913 unknown of 77011	gap of unknown length 5531 26579: contig of 1049 bp in le	of 107 unknow of 261	unknown length of 699 bp in le unknown length	gap of unknow 6 23494: contig of 104	1765: contig of 659 bp in a gap of unknown lengt	

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Query Match 96.5%; Best Local Similarity 99.1%; Matches 1634; Conservative

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PT New nucleic acid encoding U4 haematopoietin receptor superfamily PT chain - potentially useful, e.g. for modulating cell proliferation PT or immune response, for treating cancer and auto:immune disease PS Claim 1; Pages 25-26; 38pp; English.

CC This is the nucleotide sequence encoding the murine U4 protein from CC the haematopoietin receptor superfamily used in the method of the CC invention for the modulation of cell proliferation, or the immune CC response. Transformed mammalian cells are used to produce recombinant CC U4 protein. The U4 protein is used to screen for specific binding CC agents, raise antibodies. It is also used as reagents for assays and CC in pharmaceutical compositions which may modulate cell proliferation, cC cell differentiation, and the immune system (e.g. for treating immune CC deficiency, inherited or the result of infection, autoimmune diseases, CC cancer, and allergy).

So Sequence 1656 BP; 318 A; 552 C; 478 G; 308 T;
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23-UUI-1998; U00334.
15-JAN-1998; U00334.
16-JAN-1997; US-784863.
(GENY) GENETICS INST INC.
COLLINS M. DONALDSON DD, N
WPI; 98-414109/35.
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Nucleotide sequence of the murine U4 gene.
Murine: U4 protein; haematopoietin receptor superfamily;
cell proliferation; immune response; antibody; cell diff
autoimmune disease; cancer; allergy; ds.
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Claim 4; page 77-81; 182pp; English.

The haemopoletin receptor (HR) NR6.1 is a form of the novel HR NR6. Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening. Sequence 1629 BP; 336 A; 541 C; 453 G; 299 T;
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19-MAR-1998.
11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS P
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                                                                                                                                                                                                                                                                                                                                           Zhang J;
WPI; 98-260970/2
P-PSDB; W55011.
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13-FEB-1998; US-074721.
01-MAY-1997; US-850030.
13-FEB-1998; US-023890.
(ZYMO) ZYMOGENETICS INC.
Adams RL, FOSTET CC, Gilbert T
LOK S, Presnell SR, Whitmore T
WPI; 99-034662/03:
P-FSDB; W70862. New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g. down-regulating Zcytor5 natural ligands or detecting cardiotrophin-l in blood Disclosure; Page 72-75; 55pp; English. The present sequence encodes a protein designated Zcytor5, which is cDNA encoding rat zcytor5. zcytor5; down-regulation; growth factor; zcytor5; cytokinin-like receptor; down-regulation; growth factor; maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-l; cardiac pathology; heart enlargement; Zcytor5 ligand; ss. Rattus sp. V70896 standard; cDNA; 172 V70896; 17-MAR-1999 (first entry) Location/Qualifiers 159. 1436 /*tag= a /product= Zcytor5 1724 ₽₽ ΤĘ; Jelmberg Lehner

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standard; 1930 85

29-SEP-1998 (first entry)
Unspilced murine NR6 nucleotide sequence.
Haemopoletin receptor; cell proliferation; cell diff
cell survival; therapeutic; neuronal proliferation;

cell differentiation;

drug

19-MAR-1998; 11-SEP-1997; G02479. 11-SEP-1996; AU-002246. (AMRA-) AWRAD OPERATIONS I (DZIE/) DZIEGLEWSKA H E. Mus sp. W09811225-A2.

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Example 8; Page 99-100; 182ps; English.

CC NR6 is a novel haemopoletin receptor (HR). Interaction between the novel CC of a wide variety of cells. The HR and it's derivatives can be used for CC modulating the activity of the receptors e.g. to regulate development, CC maintenance or regeneration in an array of different cells and tissues in CC vitro and in vivo. They can be present in therapeutics used for CC modulating neuronal proliferation, differentiation and survival and curvival products can also be used for detection and diagnosis, e.g. for cancers CC or predisposition to cancers, or for drug screening.

SQ Sequence 1930 BP; 375 A; 623 C; 561 G; 371 T;
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Best Local Similarity
Matches 1346; Conser
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01-MAY-1998; US-0474721.
01-MAY-1997; US-045287.
01-MAY-1997; US-045287.
01-MAY-1997; US-05030.
13-FEB-1998; US-023890.
(ZYMO) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert T.
LOK S, Presnell SR, Whitmore TI
WPI; 99-034662/03.
down-regulating Zcytor5 natural in blood
                                                                                                                                                                                  cDNA encoding human Zcytor5.
Zcytor5; Cytokinin-like receptor; down-regulation; growth factor; maintenance factor; thyroid; heart; skeletal muscle; cardiotrophicardiac pathology; heart enlargement; Zcytor5 ligand; ss.
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2 13-FEB-1998; US-074721.
2 01-MAY-1997; US-045287.
01-MAY-1997; US-850030.
13-FEB-1998; US-023890.
(ZYMO) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert T.
Lok S, Presnell SR, Whitmore Ti
Disclosure; Page 68-70; 55pp; English.

The present sequence encodes an allelic varaint of protein design present sequence encodes an allelic varaint of protein design courts. Which is a cytokinin-like receptor. Soluble Zcytor5 maj administered to down-regulate the effects of a growth and/or maj factor in thyroid, heart, and skeletal muscle for example to less effect of cardiotrophin-1 on cardiac pathologies, so preventing enlargement. Zcytor5 could be used to detect cardiotrophin-1 in blood, and to discover other possible Zcytor5 ligands. A probe
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17-MAR-1999 (first entry)
cDNA encoding an allelic varaint of human 2cytor5.
2cytor5; cytokinin-like receptor; down-regulation; growth factor;
2cytor5; cytokinin-like receptor; skeletal muscle; cardiotrophin-l;
maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-l;
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Proceeding U4 haematopoietin receptor superfamily procedure and uncleic acid encoding U4 haematopoietin receptor superfamily procedure and uncleic acid encoding useful, e.g. for modulating cell proliferation. The process of the reating cancer and auto:immune disease procedure in Page 28; 38pp; English.

Convention for the nucleotide sequence encoding the human U4 protein from the haematopoietin receptor superfamily, used in the method of the convention for the modulation of cell proliferation, or the immune convention for the U4 protein is used to screen for specific binding convention. The U4 protein is used to screen for specific binding conventions, raise antibodies. It is also used as reagents for assays and convention of isolation of cognate ligands and receptors, and convention is used in pharmaceutical compositions which may modulate cell proliferation, conventions, inherited or the result of infection, autoimmune diseases, concer, and allergy).

So sequence 1579 BP; 304 A; 535 C; 473 G; 267 T;
                                                                                                                                                                                                                                                                                                                                                                                   W09831811-A1.
23-JUL-1998, U00334.
15-JAN-1998; U0-784863.
16-JAN-1997; US-784863.
(GEMY) GENETICS INST INC.
COLLINS M, DONALGSON DD, NE
WPI; 98-414109/35.
New PDBB; W59805.
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Query Match Best Local :

Similarity

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Matches 926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated haemopoletin receptor - used for for modulating proliferation, differentiation e.g. neuronal cells claim 7; Page 102-104; 182pp; English. The NR6 gene encodes a novel Haemopoletin rece
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Alexander W, Fabri L, Farle
Kojima T, Maeda M, Nash A,
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P-PSDB; W55015.
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11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
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Nucleotide sequence of clone HFK-66 encoding human
Haemopolettin receptor; cell proliferation; cell dif
cell survival; therapeutic; neuronal proliferation;
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aagccctttaacatcagctgctggtcccggaacatgaaggatctcacgtgccgctggaca
                                                                                   CACGCCCGTGACGCAGCATCCTGGCTGGCTCCTGCCTCTATGTTGGCCTGCCCCCAGAG
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Farley A, Hilton DJ, Kikuchi Y,
sh A, Nicola NA, Rakar S, Willson
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Pred. No. 1.2e-164;
0; Mismatches 124;
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Nucleotide sequence of products generated
Haemopoletin receptor; cell proliferation;
cell survival; therapeutic; neuronal proli
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(AMRA-) AMRAD OPERATIONS P
(DZIE/) DZIEGLEWSKA H E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The nucleotide sequence was generated by a 5N RACE of brain cDNA using NR6 specific primers. NR6 is a novel Haemopoietin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening. Sequence 834 BP; 167 A; 274 C; 225 G; 168 T;
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P-PSDB; W55014.
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or modulating proliferation, differentiation
rg. neuronal cells
laim 7; Page 93-95; 182pp; English.
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Matches 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells; l82pp; English.

NR6 is a novel haemopoletin receptor (HR). Interaction between the novel haemopoletin receptor (HR). Interaction between the novel haemopoletin receptor (HR). Interaction between the novel had a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, witro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.

Sequence 560 BP; 113 A; 182 C; 165 G; 100 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS PTY LTD.
(DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton
Alexander W, Fabri A, Nicola NA, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-SEP-1998 (first entry) PCR product for human NR6. Haemopoletin receptor; cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1055
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W09811225-A2.
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                                                    CATACCAACTACTCCCTCAAGTACAAGCTTAGGTGGTATGGCCAGGACAACACATGTGAG
                                                                                                                                                             AAGAACATGAAGGACTTGACCTGCCGCTGGACGCCCAGGGGCCCACGGGGAGACCTTCCTC
                                                                                                                                                                                           cggaacatgaaggatctcacgtgccgctggacaccgggtgcacacgggggagacattctta 628
                                                                                                                                                                                                                                                                                                                                                                         TCCAGGCAGCGGTCGGGGGACAACCTCGTGTGCCACGCCGGTGACGGCAGCATCCTGGCT 60
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gagtaccacactgtgggccctcactcatgccatatccccaaggacctggccctcttcact
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 452.8; DB 1
Pred. No. 2.4e-85;
0; Mismatches 67
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Rakar S, Willson
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↦

Query Match Best Local S Matches 304

Similarity

18.2%; ilarity 100.0%; Conservative

0

Score 304; DB 1; 1 Pred. No. 1.6e-54; 0; Mismatches 0;

Length

Gaps

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RESULT 12
V27142
DT V27142
AC V27142
FT CDS
FT 
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D 19-MAR-1998.

D 19-MAR-1998.

PR 11-SEP-1997; G02479.

PR (ANRA-) PARAD OPERATIONS PTY LTD.

PA (ANRA-) AMRAD OPERATIONS PTY LTD.

PA (DZIE/) DZIEGLEWSKA H E.

PA (DZIE/) DZIEGLEWSKA H E.

PA (DZIE/) M. Fabri L, Farley A, Hilton DJ, Kikuchi Y,

Alexander W, Fabri L, Farley A, Nicola NA, Rakar S, Willson
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P-PSDB; W55013.

P-PSDB; W55013.

PNew isolated haemopoletin receptor - used for developing products for modulating projiferation, differentiation and survival of cells.

PT for modulating projiferation, differentiation and survival of cells, pr e.g. neuronal cells

PT e.g. neuronal cells

Claim 6; Page 90-92; 182pp; English.

CC interaction between the novel HR and a ligand facilitates proliferation, claim 6; Construction between the novel HR and a ligand facilitates proliferation, claim for modulating the activity of the receptors e.g. claim for certain and survival of a wide variety of cells. The HR and it's claim for contact cells and tissues in vitro and in vivo. They can be present in claim for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, ce.g. for cancers or predisposition to cancers, or for drug screening.

So sequence 938 BP; 243 A; 245 C; 272 G; 178 T;
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29-SEP-1998
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receptor; cell proliferation; cell differentiation; car
l; therapeutic; neuronal proliferation; drug screening;
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Best Local Similarity
Matches 281; Conser
                                                                                                                                                                                                                                              Claim 9; Fig 3; 182pp; English.

The NR6 protein is a novel Haemopoletin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening. Sequence 11832 BP; 2447 A; 3367 C; 3298 G; 2720 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-SEP 1998 (first entry)
Nucleotide sequence for murine NR6 containing additional 5N sequence.
Haemopoietin receptor; cell proliferation; cell differentiation; cano
cell survival; therapeutic; neuronal proliferation; drug screening; s
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29-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kojima
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11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alexander W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AMRA-) AMRAD OPERATIONS PTY LTD (DZIE/) DZIEGLEWSKA H E.
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                                                                                                                                                                                                                                                                                                                                                                                                            isolated haemopoietin recomodulating proliferation, neuronal cells
                                                                                                                                 acacagctgtaatcagcccccaggaccccacccttctcatcggctcctccctgcaagcta
             atggtcgccctctgagctgtcccgctccttaacacctccaccctggccttg
                                                                       cctgctctatacatggagacacacctggggccaccgctgaggggctctactggaccctca
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ATGGTCGCCGCCTGCCCTCTGAGCTGTCCCGCCTCCTTAACACCTCCACCCTGGCCCTGG
                                                        CCTGCTCTATACATGGAGACACACCTGGGGCCACCGCTGAGGGGCTCTACTGGACCTTCA
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T, Maeda M, Nash
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sh A, Nicola NA, F
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Pred. No. 2e-49;
0; Mismatches
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Rakar S, Willson
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11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS P.
(DZIE/) DZIEGLEWSKA H E.
Alexander W. Fabri L. Fari
                                                                                                                                                                                                                                                                                                                                                                                                                                       V27145 stand
V27145;
02-OCT-1998
e.g. for
Sequence
                   New isolated haemopoietin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells
claim 8: page 108:114; 182pp; English.
That NRG gene encodes a novel Haemopoietin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's products can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for feetering and diagnosis.
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Key
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                                                                                                                                                                          P-PSDB; W55016.
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                                                                                                                                                                                                                                                                                                                                                                                      screening; ss; Mouse
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                                                                                                                                                                                                              T, Maeda M,
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 cancers or predisposition 6663 BP; 1462 A;
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/product= "1
/note= "No :
                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1182. .1744
/*tag= a
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L, Farley A, Hilton DJ, Kikuchi Y,
Nash A, Nicola NA, Rakar S, Willson
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                                                                                                                                                                                                                                                                                                                                                                                                  cell proliferation; cell therapeutic; neuronal pro
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to cancers, or for drug screening. 1852 C; 1715 G; 1634 T;
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                                                                                                                                                                                                                                                                                                                                                                                                  pll differentiation;
proliferation; drug
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                        ccctggctaaccttaatgggtccaggcagtcaggagacaatctggtgtgtcacgccc
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94
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Pred.
                                                                                                                                                            Mismatches
                                                                                                                                                                 280.4; DB 1;
No. 1.8e-49;
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Query Match
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Matches 209; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcytor5 and therapeutically to modify Zcytor5 ligand effects.

Sequence 259 BP; 53 A; 64 C; 81 G; 46 T;
                                                                                                                                                                            1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents an expressed sequence tag (EST) used to identify cDNA encoding a protein designated Zcytor5, which a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart
                              1164 cgggcccgggcggcggg 1180
                                                                                                                                                                                                                                                          1044 gcaccgtttacttcgtccaagtgcgttgtaacccattcgggatctatgggtcgaaaaagg 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 77; 55pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ZYMO) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
LOK S, Presnell SR, Whitmore TE;
WPI; 99-034662/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1997;
01-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             924 aggatttcctcttccaagccaagtaccagatccgctaccgcgtggaggacagcgggtggact 983
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V70897;
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cytor5; cytokinin-like receptor; down-regulation; gro
aintenance factor; thyroid; heart; skeletal muscle; or
                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -MAY-1998; U08865.
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                                                                                                      CCGGGATCTNGAGTGGAGCCANCCCACAGCCGGCTTCANTTCCCGCAGTGAGCGNC 239
                                                                                                                                                                                                                            GCANCGTGTACTTCGTGCAAGTGCGCTGCAANCCCTTTGGCATCTATGGCTNCAAGAAAG 179
NGGGCCCGGGNGGNGGG 256
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US-045287.
US-850030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.7%; Score 178.8; DB 1; 81.3%; Pred. No. 9.7e-29; tive 0; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oid; heart; skeletal muscle; cardiotrophin-1; enlargement; Zcytor5 ligand; EST; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Search completed: September 28, 1999, 16:45:17 Job time: 7302 sec

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Result
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Perfect score:
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1673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/PCTUS9_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-08-28-362-2
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US-08-487-811A-12
US-08-487-811A-12
US-08-487-811A-12
US-08-487-811A-11
US-08-520-678A-30
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US-08-296-624-1
US-08-296-624-1
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Ouery Match 3.2%; Score 53; DB 2; Best Local Similarity 2.1%; Pred. No. 0.0028; Matches 8; Conservative 225; Mismatches 1

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Gaps

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Length 7218;); Indels

93 ttgcagtcaccgcccgttgcgcgccacccccaatgcccgcgggtcgcccggtgcgcccgtcg 152

TELEX: 899149 ; INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 7218 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear IMMEDIATE SOURCE: CLONE: pTZ9pt-F1s US-08-232-463-14	APPLICATION NUMBER: .EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELEPHONE: (703)863-4109 TELEPHONE: (703)863-4109	US-08-232-463-14 US-08-232-463-14 Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION: APPLICANT: DORNER, F. APPLICANT: DORNER, F. APPLICANT: MOLINIER, F. APPLICANT: PALKNER, F. APPLICANT: MOLINIER, F. APPLICANT: PALKNER, F. APPLICANT: PALKNER, F. APPLICATION DATA: APPLICATION NUMBER: US/07/935,313 PRIOR APPLICATION NUMBER: US/07/935,313	38 41 2.5 198 3 US-08-330-108-16 39 41 2.5 1364 4 US-08-872-302-3 40 41 2.5 198 5 PCT-US92-10087-16 41 40.8 2.4 3047 2 US-07-927-851-2 42 40.8 2.4 6671 2 US-08-280-443-1 43 40.8 2.4 1687 2 US-08-13-219-26 44 40.8 2.4 3047 2 US-08-453-323-2 45 40.8 2.4 3047 2 US-08-440-520-2 45 40.8 2.4 3047 2 US-08-440-520-2 46 ALIGNMENTS ALIGNMENTS
			Sequence 1 Sequence 1 Sequence 2

Length 12001;

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US-08-458-568A-11/c
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CLASSIFICATION: 435

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Leary Ph.D., Kathryn R.

REGISTRATION NUMBER: 36,317

REFERENCE/DOCKET NUMBER: DFCI-0

TELECOMMUNICATION INFORMATION:

TOT PDHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/08458568A
·08-458-568A-11
                                                                                                                                                                                                       TELEFAX: (215) 568-343
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                       MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
ORGANISM: Herpes
STRAIN: Herpes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WORDPERFECT 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS: ADDRESSEE: Woodcock,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1411 YYYYYYYYYYYYYYYYYYYYYY 1433
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APPLICANT: Yeh, Lily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   333 ctggggccaccgctgaggggctctactggaccctcaatggtcgccgcctgccctctgagc 392
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APPLICATION NUMBER: US 0
FILING DATE: 05-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Philadelphia
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                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/458,568A FILING DATE: 02-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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             Herpes simplex virus
erpes Simplex Virus Type l
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                                                                                                             DNA (genomic)
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 Best Local Similarity Matches 112; Conserv
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4257 base pair
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                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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NAME: Highlander, Steven
REGISTRATION NUMBER: 37,6
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARCD:239
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/690,473 FILING DATE: 26-JUL-1996
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                                                                                                                   STRANDEDNESS:
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nucleic acid
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   Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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INHIBITOR OF APOPTOSIS
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               Score 45.4; DB 4; Pred. No. 0.11;
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Best Local Similarity
                                                                                                                       Matches
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                                                            10498
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etent No. 5834183
1534 tttggtccacatgatggtcacacttggatataccccagtgtgggtaaggttggggtattg 1593
                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 10660 base pai
                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 11:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: McCormack, Myra H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                       OLECULE TYPE:
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                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC of OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/267,803B
FILING DATE: 28-JUN-1994
                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                        TTTGATTCAAAATTTGAACAAAATTGTTTTAAATAAATTGTCTGTATACCAGTACAAGTT 10557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGCCCAGCCACACGGCGGCGGCCGCCGCGCCGCCCTGGAGG 2860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INVENTION: Type 1 and Method for Diagnosis SEQUENCES: 85
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                                                                                                                                                                                                                                                                                                 10660 base pairs
ucleic acid
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936..3384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                        linear
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                                                                                                                               Score 44; DB 4; Length 10660; Pred. No. 0.29;
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                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                     US-08-284-941-1
                                                                                                                                                                                                                   Query Match
Best Local Similarity 51.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10618 AAAAAAAAAAAAAAAAAA 10637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 843-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  FEATURE
                                                                             140 ccgggccccgtcgccaatccgcgcggcggcggcggcggcgctgtcctcgctgtggtcg 199
                                                                                                                                                                    200 cctctgttg
                                                                                                              NAME/KEY:
LOCATION:
                                                                                                                                      80 ccccataccggcgttgcagtcaccgccgttgcgcgccacccccaatgcccgcgggtcgc 139
                                                                                                                                                                                               20 gcgcccagtgacgcgcgtgcggacccgagccccaatctgcaccccgcagactcgccccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 2 Aug.
                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: NEELEY PH.D., RICHARD L. REGISTRATION NUMBER: 30092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELEFAX:
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CIGCIGCIG
                                                     GCGGGGGGCCCGGCCGGGCTTCCGGCCGCTCGCGCGTCCCTGGCGCTGGCTG 325
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                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
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FIVE PALO ALTO SQUARE
                                                                                                                                                                                                                                                                                                                                                                                                                    4403 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KIEFER, MICHAEL C
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170..3077
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334
                            208
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V: 435
                                                                                                                                                                                                                                                                                                                                                                                         double
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                                                                                                                                                                                                                                        Score 43.4; DB 4; Length 4403; Pred. No. 0.31;
                                                                                                                                                                                                                              Mismatches
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; LOCATION:
US-08-738-349-1
                                                                                                                    Query Match
Best Local
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 3529
                                                                   1665 aaaaaaaaa 1673
                                                  FORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Rel
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APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                        DRIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 3581 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                           ORGANISM:
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                                                                                                                                                                                                                                                                     ECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E OF INVENTION: Bone-Related Cadherin-Like Protein and E OF INVENTION: Process for Its Production
                                                                                                                                                                                                                                                                                              RANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASSIFICATION:
AAAAAAAA 3537
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                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08738349
                                                                                                                                                                                                                             : Mus musculus
osteoblastic cell line MC3T3E1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1300 I Street, N.W
                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                 202-408-4400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sujimura, Atsushi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           akeshita, Sunao
                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-OCT-1996
                                                                                                                                                                                                                                                                     cDNA to mRNA
                                                                                                                                                                                                                                                                                             single
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In Release #1.0, Version #1.25
                                                                                                                    76.8%;
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                                                                                                     Score 43.4; DB 4;
Pred. No. 0.3;
0; Mismatches 16
                                                                                                                               Length 3581;
                                                                                                      Indels
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RESULT

PCT-US94-03705-3

Sequence 3, Application PC/TUS9403705 GENERAL INFORMATION:

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Matches
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GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 857-0663
TELEX: 380816 COOLEY PA
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,6:
FILING DATE: 09-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: NEELEY PH.D., RICHARD L
REGISTRATION NUMBER: 30092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC'
FILING DATE: 19930309
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                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 494-7622
326 CIGCIGCIG 334
                                200 cctctgttg 208
                                                                                            140 ccgggccccgtcgcccaatccgcgcggcggcggcggcggctgtcctcgctgtggtcg 199
                                                                                                                                                                                                  146 GCGCCGCGAGCCTGTCGCCGCTATGCCTCCGCGCGCGCCCCCGCGCCCCGGGCCCCGG
                                                                 NAME/KEY:
                                                                                                                                                               80 ccccataccggcgttgcagtcaccgccgttgcgcgccacccccaatgcccgcgggtcgc 139
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                                                                                                                                                                                                                                                                      Local Similarity
les 98; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
                                                                                                                                                                                                                                gcgcccagtgacgcgcgtgcggacccgagccccaatctgcaccccgcagactcgcccccg 79
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1. PALO ALTO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4403 base pairs
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                                                                                                                                                                                                                                                                  Score 43.4; DB 5;
Pred. No. 0.31;
0; Mismatches 91;
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                                                                                                                                                                                                                                                                      91;
                                                                                                                                                                                                                                                                                                   Length 4403;
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Query Match
Best Local Similarity
Matches 68; Conserv
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                                                                              APPLICANT: Gaynor, Rich
APPLICANT: Wu, Foon W.
TITLE OF INVENTION: Cel
TITLE OF INVENTION: and
TITLE OF INVENTION: Tre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 05-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Di
                                                                                                                                                                                                                                                                                   855 GGCTGCGGCTGCTGCTGCTGCTACCGCTGCTGTGGCTACTGGTGCT 903
                                                                                                                                                                                                                                                                                                                                                   795 CAGCCCTGTTCGCGCTCTCGGCAGTGCCGGGGGGGGCGCCCTCCCCCATGCCGCCCTCCG 854
                                                                                                                                                                                                                                                                                                                 162 cgcggcggccgcgcggcgctgtcctcgctgtggtcgcctctgttgct 210
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ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                 DRRESPONDENCE
                                                                 IMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
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SOFTWARE: WordPer
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                                 ADDRESSEE:
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                                                                                                                                                                       INFORMATION:
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Houston
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                                                                                                                                                Gaynor, Richard B
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mark A. Perrella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mu-En Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            I: 3.5" Diskette, 1.44 Mb
IBM PS/2 Model 50Z or 55SX
SYSTEM: MS-DOS (Version 5.
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                                              ADDRESS
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                                                                                Cellular Nucleic Acid and Uses Thereof in reTreatment of AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                            2.6%;
                              White & Durkee
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ER: 05433/007001
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Pred. No. 0.28;
0; Mismatches 41;
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                                                                                                                                                                                                                                                                                                                                                                                                                         41;
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                                                                                          Gene Expression and in the
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Best Local S
Matches 51
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                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,7
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                ITLE OF INVENTION: NOVEL CATHEPSIN AND METHODS AND ITLE OF INVENTION: COMPOSITIONS FOR INHIBITION THEREOF UMBER OF SEQUENCES: 20
                                                                                                                                                                   ADDRESSEE: ATHENA NEUROSCIENCES
STREET: 800 F. Gateway Blvd.
CITY: South San Francisco
                                                                                                                            COUNTRY: U
                                                                                                                                                                                                    ADDRESSEE:
                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
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STRANDEDNESS: single
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                                                                                                                                          USA
                                                                                                                                                                                                                                                                             CHRYSLER, SUSANNA
                                                                                                                                                                                                                                                                                                               TATSUNO, GWEN
                                                                                                                                                                                                                                                                                                                             MCCONLOGUE,
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MBER: US/08/467,607
06-JUN-1995
                                                                                                                                                                                                                                                                                                                                          SUKANTO
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Pred. No. 0.36;
0; Mismatches 13;
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REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:

002010-007

CLASSIFICATION:

ORNEY/AGENT INFORMATION:

DUVALL,

JEAN M.

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; NAME/KEY:
; LOCATION:
US-08-467-607-2
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                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 877-0900
                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30
ELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                     STREET: 800 r. Garantisco
CITY: South San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                    COUNTRY: UZIP: 94080
                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPOLOGY:
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                REGISTRATION NUMBER: 32,73:
                                                                                                         APPLICATION NUMBER:
                                                                            CLASSIFICATION:
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                                             DUVALL,
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103..1011
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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0 F. Gateway Blvd.
                                                                          06-JUN-1995
ON: 514
                                                             INFORMATION:
                                             JEAN M.
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                                                                                                           US/08/469,362
                                                                                                                                                                                                                                                                                                                                              CATHEPSIN AND METHODS AND SITIONS FOR INHIBITION THEREOF
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                 002010-005
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US-08-469-362-2
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              NEORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                              ELECOMMUNICATION INFORMATION TELEPHONE: (415) 877-0900
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SOFTWARE: PatentT
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                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/850,392
                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                             REGISTRATION NUMBER:
ENGTH:
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103..1011
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linear
                                              (415)
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                                                                                                                                                                                                                                                                                  IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             base pairs
                                                                                                                                                           06-JUN-1995
                                                                                                                          JEAN M.
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49.6%; Pred. No. 0.29;
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                                                                                                                                                                                                                                                                     Release #1.0, Version #1.30
                                                                                                                                                                        US 08/469,362
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; LOCATION:
US-08-850-392-2
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Best Local Similarity
Matches 67; Conserv
                                                                                                                                            NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1493
                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 289 base pairs
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                            ORIGINAL SOURCE:
                                             MOLECULE TYPE:
                                                                                                                                                                                            TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                TELLEFAX: 148345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: PO Box /*/
CITY: Falls Church
                ORGANISM:
                                                                                                                                                                                                                              NAME: Murphy Jr, Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 36
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 22-NO
                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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|AAAAAAAAAAAAAAA 1507
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                                                                                               nucleic acid
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QM9414
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                                                                                                                                                                           : (703) 205-8000
(703) 205-8050
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Marjatta, Ranua
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                                                             linear
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103..1011
             Trichoderma reesei
                                               CDNA
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                                                                              single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.6%; Score 43; DB 4; Length 1558; 49.6%; Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pulps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mannanase enzymes, genes coding for them, methods for isolating the genes, and methods for bleaching light
                                                                                                                                                                                                                                                                                                                          US/08/341,568
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RESULT 14
US-08-911-020-3
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Matches 8
                                                                                                               TELEFAX: .(703) 205-805
TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                           FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA
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                                                                                                                                                                                      REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 365-262P
REFERENCE/DOCKET NUMBER: 365-262P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 GATTTGATGAAGAATATGACATTGCATGCCTGCTACATACGTAGATTATGATTGGGGGAG 191
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                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: PO Box 747
CITY: Falls Church
                                                                                                                                                                                                                                                              APPLICATION NUMBER: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 22040-0747
               ORGANISM:
                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                   ENGTH:
                                                                                                                                                                          ELEPHONE:
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LE OF INVENTION:
                                                                                                                                                                                                                    ISTRATION NUMBER:
                                                                                    nucleic acid
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Similarity 56.3%;
80; Conservative
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1: Trichoderma reesei
QM9414
                                                                                                289 base pairs
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PO Box 747
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Siika-aho, Matti
Viikari, Liisa
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                                                      linear
                                                                                                                                                                                                                                                                                                                                                                   PatentIn
                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                           (703)
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13-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                           CDNA
                                                                                                                                                                                                                                  Jr, Geral
                                                                     single
                                                                                                                                                            205-8050
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Pred. No. 0.21;
0; Mismatches 62
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ing the genes, and metl
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Query Match 2.6%; Best Local Similarity 56.3%;

Score 42.8; DB 4; Pred. No. 0.21;

Length 289;

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                                                                                                                                                             FORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                             FILING DATE: September 29, TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA
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                                                        OLECULE TYPE: DI
IYPOTHETICAL: NO
DRIGINAL SOURCE:
                                                                                                                                                                                                                                    ELECOMMUNICATION INFORMATION:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                REGISTRATION NUMBER: 22,798
REFERENCE/DOCKET NUMBER: 204/139
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                                          NDIVIDUAL ISOLATE:
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: CA
:RY: USA
                                                                                                                            nucleic acid
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                                                                                                                                                                                                                                                                                                                                                       ION NUMBER:
                                                                                                                                                                                                       (213) 489-1600
(213) 955-0440
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                                                                        linear
E: DNA (genomic)
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Katze, Michael G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lyon & Lyon
1 West Sixth Street
                                                                                                                 double
                                                                                                                                                                                                                                                                             E. Olson
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                                         HUMAN PKR GENE, FIGURE 5
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US-08-143-219-1

Query Match 2.5%; Score 42.6; DB 2; Length 2628; Best Local Similarity 84.2%; Pred. No. 0.41; Matches 48; Conservative 0; Mismatches 9; Indels 0; Gaps

0

Search completed: September 28, 1999, 16:39:36
Job time: 6962 sec

B 5

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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd
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OM nucleic - nucleic search, using sw model September 28, 1999, 16:44:42; Search time 303.81 Seconds (without alignments)
1377.741 Million cell updates/sec

92:

Title: Perfect score: US-09-037-657-14 1673 1 ggcacgagcttcgc

Sequence: ggcacgagcttcgctgtccg...aaaaaaaaaaaaaaaaa 1673

Scoring table: IDENTITY_NUC

Database : N_Geneseq_36:* 311585 seqs, 125096042 residues

and is score Pred. No. No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, serived by analysis of the total score distribution.

SUMMARIES

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2.7 114955
2.7 12001
X53491
Q76213
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Human adenosine . HSV L/ST region.

ALIGNMENTS

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M W09811225-A2.

D 19-MAR-1998.

PF 11-SEP-1997; G02479.

PR 11-SEP-1996; AU-002246.

PA (AMRA-) AMRAD OPERATIONS PTY LTD.

PA (DZIE/) DZIEGLEWSKA H E.

PA (DZIE/) DZIEGLEWSKA H E.

Alexander W, Fabri L, Farrley A, Hilton DJ, Kikuchi Y,

Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
       The haemopoletin receptor (HR) NR6.2 is a form of the novel HR NR6. Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening. Sequence 1673 BP; 344 A; 550 C; 474 G; 305 T;
                                                                                                                                                              e.g. neuronal cells
Claim 5; Page 84-87; 182pp; English
The haemopoletin receptor (HR) NR6.
                                                                                                                                                                                                                   New isolated haemopoletin receptor - used for developing products for modulating proliferation, differentiation and survival of cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel haemopoietin receptor NR6.2 gene. Haemopoietin receptor; cell proliferaticell survival; therapeutic; neuronal pr
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ğ 밁 Ş å 밁 á B Ş 밁 Š Query Match Best Local Similarity Matches 1673; 181 241 999agcccacacagctgtaatcagcccccaggaccccacccttctcatcggctcctccct 300 121 181 121 61 61 GCTGTCCTCGCTGTGGCCTCTGTTGCTCTGTGTCCTCGGGGTGCCTCGGGGCGGATC 240 cccaatgcccgcgggtcgcccgggccccgtcgcccaatccgcgcggcggccgccgcgggcc 180 GGCACGAGCTTCGCTGTCCGCGCCCAGTGACGCGCGTGCGGACCCGAGCCCCAATCTGCA 60 ggcacgagcttcgctgttccgcgcccagtgacgcgcgtgcggacccgagccccaatctgca 60 Conservative 100.0%; 0 Score 1673; Pred. No. 0; Mismatches DB 1; 0; Length 1673; Indels 0 Gaps 300

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301 gcaagctacctgctctatacatggagacacacctggggccaccgctgaggggctctactg 360

COUNT

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RESULT 14
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ORGANISM
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Best Local S
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                         Rattus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

1 (bases 1 to 470)

Lee, N.H.; Glodek, A.; Chandra, I.; Mason, T.M.; Quacker
                                                                                                                                                            AI233311 470 bp
EST229999 Normalized
RKIDD49 3' end, mRNA
            Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.
                                                                                            Rattus sp.
                                                                                                                         AI233311.1
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/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin registant)"
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sequence.
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REFECENCE

TITLE

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Vertebrata;

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DEFINITION ACCESSION

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KEYWORDS
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COMMENT
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ORIGIN
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                                                           93397623
AI071408.1
                                                                                        AI071408 464 bp mRNA EST UI-R-C2-nb-d-08-0-UI-S1 UI-R-C2 Rattus norvegicus UI-R-C2-nb-d-08-0-UI 3', mRNA sequence. AI071408
Norway rat.
Rattus norvegicus
Eukaryota; Metazoa
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Tel: (301)-838-3529
Fax: (301)-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene Index
Unpublished (1998)
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Seq primer: M13-21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Rattus sp."
/db_xref="taxon:10118"
/clone="RxIDD49"
/clone_lib="Normalized rat kidney, Bento Soares"
/note="Organ: kidney; Vector: pT7T3Pac; Site_1:
Site_2: NotI"
143 c 124 g 115 t
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Center Drive, Rockville,
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Chordata;
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Pred. No. 1.2e-52;
0; Mismatches 41
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RESULT 1
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BASE COUNT
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High quality sequence stop: 431.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL IMAGE Consortium (info@image.linl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          National Cancer Institute, Cancer Geno
Tumor Gene Index
Unpublished (1997)
On Aug 21, 1998 this sequence version
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Eutheria; Primates;
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National Cancer Institute, Cancer Genome Anat
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                    69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Robert_Strausberg@nih.gov
                                                                        double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified PT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed
                   from the same fetus as the fetal heart library, fetal heart NbHH19W." 175 c 128 g 74 t 1 others
                                                                                                                                                                                /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/clone-"IMAGE:1741228"
                                                                                                                                                                                                                                                                           'dev_stage="19 weeks"
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sapiens cDNA clone
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RESULT 13
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Best Local Similarity 84.1
Matches 376; Conservative
                                                                                                                                                                                                       JOURNAL
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                                                                               Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                      Tumor Gene Index
Unpublished (1997)
On Jan 14, 1998 this sequence version
                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Eutheria; Primates; Catarrhin;
1 (bases 1 to 431)
                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
                                        High quality sequence stop: 407
Location/Qualifiers
                                                                                                                                                                                                                                  National Cancer Institute,
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National Cancer Institute, Cancer Genome Anatomy
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                                                                      primer: -40UP from Gibco
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 1.1e-54;
0; Mismatches 71;
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gacattottacataccaactactcoctcaagtacaagct 657
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                                                                                              CATCCTGGCTGCCTGCCTCTATGTTGGCCTGCCCCCAGAGAAACCCGTCAACATCAG
                                                                                                               cattotggctggctcctgcctctatgttggcttgccccttgagaagccctttaacatcag 558
                                                                                                                                                      CCTCAATGGGTCCAGGCAGCGGTCGGGGGACAACCTCGTGTGCCACGCCCGTGACGGCAG
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Email: Robert 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 466)
NCI-CGAP http://www.ncbi.nlm.nlh.goy/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced g1:2151491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: Robert_Strausberg@nih.gov
This clone is available royalty-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D
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/db_xref="taxon:9606"
/clone="IMAGE:1741879"
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/dev_stage="19_weeks"
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85.6%;
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Pred. No. 1.8e-58;
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                                                         GCACGAGGAGTTCCTCGGCTGGCTCAAGAAGCACGCATACTGCTCGAACCTTAGTTTCCG 64
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W17583 390 bp mRNA mb75b01.rl Soares mouse p3NMF19.5 IMAGE:335209 5', mRNA sequence.
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The WashU-HHMI Mouse EST Project
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Pred. No. 1.8e-56;
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NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Pro
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                   Unpublished (1997)
On Jan 19, 1998 this sequence version
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                                                                                                           Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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                                                                                    AI185780 (qe44h04.x1 Soa)
IMAGE:1741879
                                                               AI185780
g3736418
Homo sapiens
Eukaryota; Metazoa;
Eutheria; Primates;
                                                     AI185780.1
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/map="839C02; 821G11; 4;
/clone="IMAGE:1705398"
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                                                                                  400 DD MRNA ES
Soares_fetal_lung_NbHL19W Homo
379 3', mRNA sequence
                                                      GI:3736418
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Chordata; Craniata;
Catarrhini; Hominida
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Pred. No. 1.8e-58;
D; Mismatches 66
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cotgocototgagotgtocogocotocttaacacotocacoctggccotggccotggctaa 438
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Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project
Tumor Gene Index
Unpublished (1997)
On Feb 17, 1998 this sequence version replaced g1:2150926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 467.
Location/Qualifiers
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/dev_stage="19_weeks"
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Pred. No. 3.7e-60;
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1 (bases 1 to 462)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurola Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Lou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         £1394468 462 bp mRNA EST 30-MAR-1999 £179d12.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2105495 3',
                                                                                                                                                                                                                                                                                                                          Insert Length: 1631
                                                                                                                                                                                                                                                                                                                                                           www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
Cound through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: M. Bento Soares, Ph.D.,
sonaldo, Ph.D.
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/clone="IMAGE:2105495"
/clone=11b="NCI_CGAP_Brn23"
/tlssue_type="911oblastoma (pooled)"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 474)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)

On Apr 7, 1998 this sequence version replaced g1:3034955.
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Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Lou
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/lab_host="DH10B"
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 445)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA039053 445 bp mRNA m199d07.rl Soares mouse embryo NbME13.5 clone IMAGE:474733 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4444 Forest Park Parkway, Box 8501,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The WashU-HHMI Mouse EST Project Unpublished (1996)
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/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
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/clone="IMAGE:474733"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                         /sex="unknown"
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                                                            Score 430.6; DB 27; Pred. No. 4.3e-73; 0; Mismatches 9;
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                                                                                                                                                     Email: msoares@blue.weeg.ulowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.
Fatima Bonaldo, Ph.D. Clone distribution: clones will be available
                                                                                                                                                                                                                      Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iow Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA866388 428 bp mRNA EST 05-FEB-1999 UI-R-A0-aj-f-04-0-UI-S3 UI-R-A0 Rattus norvegicus cDNA clone UI-R-A0-aj-f-04-0-UI-S3 UI-R-A0-aj-k-04-0-UI-S similar to gb|Ac003112|AC003112 Human from chromosome 19 specific cosmid R30292, genomic sequence,
                                                                                                                                                                                                                                                                                                                              On Mar 16, 1998 this sequence version replaced
                                                                                                                                                                                                                                                                                                     Contact: Soares,
                                                                                                                                                                                                                                                                                                                                                     Genome Res. 6 (9), 791-806 (1996)
97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                              ough Research Genetics primer: M13 Forward.
/organism="Rattus norvegicus"
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/db_xref="taxon:10116"
/map="between D1151765 and UGB"
/clone="UI-R-A0-a)-f-04-0-UI"
/clone_1ib="UI-R-A0"
                                                                                                             Location/Qualifiers
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BASE COUNT
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AA049278/c
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Best Local Similarity
Matches 470; Conserv
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                                                                                            Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases I to 503)
I (bases I to 503)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                      AA049278 503 bp mRNA
mj45c04.rl Soares mouse embryo NbME13.5
clone IMAGE:479046 5', mRNA sequence.
AA049278
g1755309
Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project
                                              The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Dec 30, 1996 this sequence ve
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                                                                                                                                                                                                                                           house mouse.
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                                               sequence version
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Pred. No. 2.8e-78;
0; Mismatches
                                               replaced
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                                                                                                                                                                                                                                                                                             quality sequence
mouseest@watson.wustl.edu
                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="IMAGE:479046"
/clone_lib="Soares mouse
                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                               try sequence stop:
                                                                                                                                                                     /tissue_type="embryo"
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                                                                                                                                                                                               /sex="unknown
                                                                                                                                                        lab_host="DH10B"
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87 ctgggcaacaaagaaacctaccagaggctggggcacaatgagctcccacaaccaccacctt gccatcctcctgctgggtcagacctggaggctcacctgaattggagcccctctgtaccat acgaccagtggcgtgcttggatgcagaagtcacacaagacccgaaaaccaggacgagggga agcagttcctcggctggctcaagaagcacgcatactgctcgaaccttagtttccgcctgt gcgagtggagccaccccaccgctgcctccacccctcgaagtgagcgcccgggcccgggcg GCGGGGTGTGC-CGACGCGGGGGGGGGGGGGA-CCCAGCTCGGGCCCGGTGCGGCGCGAGCTCA TCCTGCCCTCGGGCAGACGGGGTGCGGCGAGAGGTCCTGCCGGCTAAACTCTAAGGATAG ACGACCAGTGGCGTGCTTGGATGCAGAAGTCACAAGACCCGAAACCAGGACGAGGGGA AGCAGTTCCTCGGCTGGCTCAAGAAGCACGCATACTGCTCGAACCTTAGTTTCCGCCTGT al Similarity 497; Conserv Conservative 26.9%; Score 449.4;
Pred. No. 1.1e
0; Mismatches 0 ..1e-76; DB 29; σ, Length 4; Gaps 1415 208 1235 1535 1475 1355 1295 1175 88 148 328 386 28 268 4

REFERENCE AUTHORS

ACCESSION

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AUTHORS
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                                          gctgctggtcccggaacatgaaggatctcacgtgccgctggacaccgggtgcacacgggg
ccctcttcactccctatgagatctgggtggaagccaccaatcgcctaggctagcaagat
                                                                                                                                                            GCTGCTGGTCCCGGAACATGAAGGATCTCACGTGCCGCTGGACACCGGGTGCACACGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l (bases 1 to 464)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Ld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
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Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                           30, 1996 this sequence version
                                                                                                                                                                                                                                                                                                          M.Fatima Bonaldo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:479043"
/clone_lib="Soares mouse embryo NbME13.5 14.5"
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                                                                                                                                                                                                                    Score 464; DB 29;
Pred. No. 1.9e-79;
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W66776 482 bp mRNA EST 14-JUN-1996 mel7b11.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone TWAGE: 387741 5' similar to PIR: B38252 B38252 granulocyte colony-stimulating factor receptor precursor; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Marra M/Mouse EST project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g1375694
W66776.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W66776
                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Apr 14, 1993 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque, Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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GI:1375694
                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                             /sex="unknown"
                                                                                                                                      'clone_lib="Soares mouse embryo NbME13.5
                                                                                                                                                           'clone-"IMAGE:387741"
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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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OM nucleic - nucleic search, using sw model
Run on: September 28, 1999, 15:38:03

September 28, 1999, 15:38:03; Search time 2095.87 Seconds (without alignments) 1574.548 Million cell updates/sec

Title: US-09-037-657-14
Perfect score: 1673
Sequence: 1 ggcacgagcttcgctgtccg

Scoring table: IDENTITY_NUC

Searched: 2546578 seqs, 986266752 residues

Database : EST:*
1: em_est1:*

5: em_est5:*
6: em_est5:*
7: em_est7:*
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20: gb_est1:*
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40: gb_est21: *
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43: gb_est25: *
44: gb_est26: *
45: gb_est26: *
46: gb_est27: *

49: gb_est30:*
50: gb_est31:*
51: gb_est32:*
52: em_est20:*

54: em_est22:*
55: em_est23:*
56: em_est24:*
57: em_est25:*
58: em_est26:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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9564 EST1923	05 mc69e09.	357868 qv13b02	417616 tg80c0	64328 q109c05.	014965 mh23e02	374006 SWOVAFCA	121532 zk89c11.	927378 om27a0	127694 zk89c11.	2128 om45e12.	535068 UI-R-C3	8873 zb17h05.	4009 EST00035	377893 EST905	925924 UI-R-A1-	074921 oy04d08	011309 AV0113	010798 AV01079	407 ym88d09.s	6604 zc32h10.s1	043001 zk56f01.	575060 UI-R-GO-	A270365 va63h12	V032198 AV0321	A042914 zk56f01.	670108 we65f03.	4687 UI-R-GO-	579568 di-R-GO-	269388 q126b05.	071408 UI-R-C2-	AI233311 EST229999	1333813 me38403.	1/583 mb/5bul.rl	I185780 ge44h04.	1002 gb69g04	1394468 tf79d12.	.1185924 qe50c05.	421423 tf25h01.	866388 UI-R-AO-	.A039053 mi99d07.	A049278 mj45c04	6776 me17b11.	49280 mj45d0	nescription	224544	

ALIGNMENTS

RESULT 1

AA049280

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REFERENCE
AUTHORS
TITLE
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MEDLINE
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Best Local Similarity
                                                                                                                                                                                                                                                         Matches
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                                                                            tactgctcgaaccttagtttccgcctgtacgaccagtggcgtgcttggatgcagaagtca 1327
             403;
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Program for Rat Gene Discovery and Mapping
University of Iowa
451% Brokstein Medical Research Building Iowa City, IA 52242, USA
Tel? 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                           purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C2 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research (791-806, 1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UT-R-C2) was constructed as follows: PCR amplified cDNA inserts from UT-R-C1 clones from which 3' ESTs had been derived was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 used as a driver in a hybridization with the UI-R-C1
library in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library) was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Rattus norvegicus"
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ary is a subtracted library derived from the
ary, which is a subtracted library derived ir
-c0 library. The UI-R-C0 library consisted o
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Pred. No. 9.1e-52;
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                                                                                                      gctggggcacaatgagctcccacaaccacagctttggtccacatgatggtcacacttgga
                   TGTACCCCAATATGGGTAGGGTTGGAGTAATGACAAGGGTTATGCAGGACCCTCCAAGAG 45
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Search completed: September 28, 1999, 15:38:09 Job time: 3277 sec

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Result
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/5D_COMB.seq:*
/cgn2_6/ptodata/2/ina/Dackfiles1.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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 PCT US93-02147A-1
PCT US94-03705-3
US-08-2467-607-2
US-08-467-607-2
US-08-469-362-2
US-08-341-568-3
US-08-911-020-3
US-08-911-020-3
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US-08-911-020-3
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PCT US96-10521-14
PCT US96-10521-17
US-08-056-051-5
US-08-08-611-12
US-08-928-611-12
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US-08-458-568A-11

US-08-690-473-1

US-08-267-803B-8

US-08-284-941-1

US-08-738-349-1
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Query Match 3.2%; Score 53; DB 2; Length 72 Best Local Similarity 2.1%; Pred. No. 0.0028; Matches 8; Conservative 225; Mismatches 150; Indels	RESULT 1 US-08-232-463-14	38 41 2.5 198 3 US-08-330-108-16 39 41 2.5 1364 4 US-08-872-302-3 40 41 2.5 198 5 PCT-US92-10087-16 41 40.8 2.4 3047 2 US-07-927-881-2 42 40.8 2.4 6671 2 US-08-280-243-1 43 40.8 2.4 1687 2 US-08-443-129-26 44 40.8 2.4 3047 2 US-08-443-323-2 45 40.8 2.4 3047 2 US-08-440-520-2 ALIGNMENTS
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US-08-458-568A-11
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                                                                                                                                                                                 TELEFAX: (215) 568-343 (INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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tent No. 5821339
                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTI-SENSE:
                                                                              OLECULE TYPE: DI
                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: DF
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NAME: Leary Ph.D., Kathryn R.
REGISTRATION NUMBER: 36,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITLE OF INVENTION: Composition Infections
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/458,568A FILING DATE: 02-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 0 FILING DATE: 05-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                STRANDEDNESS:
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DEDNESS: double
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                                                SOURCE:
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          Herpes Simplex Virus Type 1
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                               Herpes simplex virus
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Place, 46th
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                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: ARC
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                         NAME: Highlander, Steven REGISTRATION NUMBER: 37,6
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 26-JUL CLASSIFICATION: 435
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                 2 gcacgagcttcgctgtccgcgcccagtgacgcgcgtgcggacccgagccccaatctgcac 61
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Similarity
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Similarity 50.2%;
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                                                                                                                                                                        nucleic acid
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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INHIBITOR OF APOPTOSIS
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                                                          Mismatches
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JS-08-267-803B-8
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Best Local Similarity
Matches 80; Conser
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1534 tttggtccacatgatggtcacacttggatataccccagtgtggggtaaggttggggtattg 1593
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 10660 base bas
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 28-JUN-1994 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
                                                                                                                                                                                                                                             NAME/KEY:
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PERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                               CULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                            ERENCE/DOCKET NUMBER: 110
                                                                                                                                                                                                                                                                                                          NDEDNESS:
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                                                                                                                                                                                                                                                                                                                         : 10660 base pairs nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McCormack, Myra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INVENTION: Type 1 and Method for Diagnosis F SEQUENCES: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08267803B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Mueting, Raasch, Gebhardt & Schwappach, P.A. P.O. Box 581415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nneapolis
                                                                                                                                                                                                                                                                                                                                                                                            612-305-1228
                                                                                                                                                                                                                         CDS
936..3384
                                                                                                                               Conservative .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chung, Ming-yi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ranum,
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                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                               DNA
                                                                                                                                                                                                                                                                                                           single
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                                                                                                                                              2.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene Sequence for Spinocerebellar Ataxia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/267,803B
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                                                                                                                                                                                                                                                                                                                                                                                                                                           110.00030120
                                                                                                                           Score 44; DB 4; Length 10660;
Pred. No. 0.29;
0; Mismatches 60; Indels
                                                                                                                           Gaps
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; LOCATION:
US-08-284-941-1
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Best Local 9
                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tent No.
                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1654 аапапапапапапапапапапа 1673
                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: NEELEY PH.D., RICHARD L.
REGISTRATION NUMBER: 30092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                        266
                                                                                   140
                                                                                                                                                                    200 cctctgttg 208
                                                                                                            y Match 2.6%;
Local Similarity 51.9%;
hes 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITLE OF INVENTION:
                                                                                                                                    80 ccccataccggcgttgcagtcaccgccgttgcgcgccacccccaatgcccgcgggtcgc 139
                                                                                                                                                                                          20 gcgcccagtgacgcgcgtgcggacccgagccccaatctgcaccccgcagactcgccccg 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 2 Augu
CIGCIGCIG 334
                                                     GCGGGGGGCGCCGGGCCCGGGTTCCGGCCCCTCGCGCCGTCCCTGGCGCTGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMUNICATION INFORMATION:
                                                                             ccgggccccgtcgccaatccgcgcggcggcgccgcggcggcgctgtcctcgctgtggtcg 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              380816 COOLEY PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: COOLEY GODWARD CASTRO HUDDLESON & TATUM FIVE PALO ALTO SQUARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                CDS
170..3077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (415)
                                                                                                                                                                                                                                                                                                                                                                                        double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            843-5070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/284,941
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                                                                                                                                                                                                                           Score 43.4; DB Pred. No. 0.31; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Version #1.25
                                                                                                                                                                                                                                                       DB 4; Length 4403;
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08-738-349-1

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                NFORMATION FOR SEQ ID NO:
                           1665 aaaaaaaaa 1673
                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 3581 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                              DRIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         ELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                          ECULE TYPE:
                                                                                                                                                                                                                                                                                                                     RANDEDNESS: single
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AAAAAAAAA 3537
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                                                                                                                 Conservative
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284..2671
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                                                                                                                                                                                                                                                             Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cakeshita,
                                                                                                                                                                                                                                                                                                          Linear
                                                                                                                                                                                                                                                                                                                                                                                                            202-408-4000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                                                                                          cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-1996
                                                                                                                             2.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Makoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bone-Related Cadherin-Like Protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Release #1.0, Version #1.25
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                                                                                                              Score 43.4; DB Pred. No. 0.3; 0; Mismatches
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                                                                                                               16;
                                                                                                                                         4;
                                                                                                                                         Length 3581;
                                                                                                               Indels
                                                                                                              0;
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RESULT

RESULT

PCT-US94-03705-3

Sequence 3, Application PC/TUS9403705 GENERAL INFORMATION:

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LOCATION:
PCT-US93-02147A-1
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                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 380816 COOLEY PA
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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APPLICATION NUMBER: PC
FILING DATE: 19930309
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                        200 cctctgttg 208
                                                                                             140
                                                                                                                                                                                        326 CIGCIGCIG
                                                             266 GCGGGGGCGCCGGGCCCGGGTTCCGGCCGCCGCCGCGTCCCTGGCGCTGGCTG
                                                                                                                         80 ccccataccggcgttgcagtcaccgccgttgcgcgccacccccaatgcccgcgggtcgc 139
                                                                                                                                                                                                                   20 gcgcccagtgacgcgcgtgcggacccgagccccaatctgcaccccgcagactcgccccg 79
                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: NEELEY PH.D., RICHARD L
REGISTRATION NUMBER: 30092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LECOMMUNICATION INFORMATION: TELEPHONE: (415) 494-7622
                                                                                                                                                                                                                                                                                                                                                                                                                      COPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPLICATION NUMBER: US 0
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                                                                                        ccgggccccgtcgcccaatccgcgcggcggcgccgcggggcgctgtcctcgctgtggtcg 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEFAX:
                                                                                                                                                                                                                                                    2.6%;
1 Similarity 51.9%;
98; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94306
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CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIVE PALO ALTO SQUARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4403 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.25
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170..3077
                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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334
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                                                                                                                                                                                                                                                                                                                                                                                                  DNA (CDNA)
                                                                                                                                                                                                                                                                                                                                                                                                                                   double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPOSITIONS AND METHODS FOR PACE 4 AND PACE 4.1 GENE AND POLYPEPTIDES IN CELLS
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                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                    DB 5;
                                                                                                                                                                                                                                                      91;
                                                                                                                                                                                                                                                                                      Length 4403;
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                                                                                                                                                                   Patent No. 5677143
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Best Local Similarity
Matches 68; Conserv
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ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 FL

MEDIUM TYPE: 1BM PS/2 Model 50Z or 55SX

TOTAL MS-DOS (Version 5.0)

TOTAL MS-DOS (Version 5.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                        CORRESPONDENCE ADDRESS
                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                 162 cgcggcggccgcggcgctgtcctcgctgtggtcgcctctgttgct 210
                                                                                                                                                                                                                                                                                                              102 ccgcccgttgcgccacccccaatgcccgcgggtcgcccggggccccgtcgcccaatccg 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTORNEY/AGENT INFORMATION:
                                                                                                   TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: Reg
                                            DDRESSEE:
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                                                                                                                                                                                                                                                       GGCTGCGGCTGCTGCTGCTACCGCTGCTGTGGCTACTGGTGCT 903
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                                                                                                                                                            INFORMATION:
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Houston
: TX
                                                                                                                                                                                     Application US/08242677
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                            P.O. Box 4433
                                                                                                                              Wu, Foon W
                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225 Franklin
                                                                                                                                          Gaynor, Richard B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                           Arnold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER: PCT/US94/03705
5 April 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fraser
                                                                                                                                                                                                                                                                                                                                                                                          2.6%;
                                                                           Cellular Nucleic Acid Binding Protein and Uses Thereof in regulating Gene Expression and in the Treatment of AIDS
                                         White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYNTHASE GENE
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                                                                                                                                                                                                                                                                                                                                                                                       Score 43.4; DB 5; Pred. No. 0.28;
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US-08-242-677-1
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                                                                                                                                                                                                                                                                                                                                                                          quence 2,
                          CURRENT APPLICATION DATA:
                                                                                 MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                               5133 AAAA 5136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L
REGISTRATION NUMBER: 33,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                  PPLICANT:
                                                                                                                                                                                                                                                                         PPLICANT:
                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                        ITLE OF INVENTION: NOVEL CATHEPSIN AND METHODS AND THEREOF
                                                                                                                                                      STREET: 800 F. Gateway Bl'CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
APPLICATION NUMBER: US/0
FILING DATE: 06-JUN-1995
                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 5173 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
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                                                                                                               94080
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                                                                                                                                          CA
                                                                                                                                                                                                ENCE ADDRESS
                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                SINHA, SUKANTO
MCCONLOGUE, LISA
                                                                                                                                                                                                                                                      ANDERSON, JOHN
CHRYSLER, SUSANNA
                                                                                                                                                                                                                                                                                   TATSUNO, GWEN
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                                                                                                                                                                     ATHENA NEUROSCIENCES

OF. Gateway Blvd.
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA
           US/08/467,607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Release #1.0, Version #1.25
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33,732
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                                         Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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CLASSIFICATION:

ORNEY/AGENT INFORMATION:

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; LOCATION:
US-08-467-607-2
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Best Local Similarity
Matches 67; Conser
INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-469-362-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1433 TCCCCMTCCCCCCANTGNTGRAWAAARAATCTGCCCCTYCCCGAAAAAAAAAAAAAAAAAA 1492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1373 TCMCCATTCTTATTTCACYTTAGRATCMAGGGTGGGRGRGRGRGGGGAGGGAATTGTCART 1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1659 aaaaaaaaaaaaaa 1673
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                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 877-0900
                          REGISTRATION NUMBER: 32,731
REFERENCE/DOCKET NUMBER: 00
ELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 877-0900
                                                                                                         TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               ORRESPONDENCE ADDRESS
                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                         APPLICATION NUMBER: US/08/469,362 FILING DATE: 06-JUN-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 32,731 REFERENCE/DOCKET NUMBER: 00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                               DDRESSEE:
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                                                                                                                                                                                                                                                                     94080
                                                                                                                                                                                                                                                                                                 South San Francisco
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                                                                                            DUVALL,
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                                                                                                                                                                                                                                                                                                                                   800
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                                                                                                                                                                                                                                                                                  USA
                (415
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0 F. Gateway Blvd.
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                                                                                            JEAN M.
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                                                                                                                                                                                                                                                                                                                                                                                                                            CHRISTOPHER M.F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.6%; Score 43;
49.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                             COMPOSITIONS FOR
                                                                                                                                                                                                                                                                                                                                                                                                            NOVEL CATHEPSIN AND METHODS
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; NAME/KEY:
; LOCATION:
US-08-469-362-2
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Best Local
              TELEFAX: (415)
INFORMATION FOR SEQ
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SEQUENCE CHARACTERISTICS:
                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                            ORRESPONDENCE
                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1558 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                            REFERENCE/DOCKET NUMBER: 00
LECOMMUNICATION INFORMATION:
TELEPHONE: (415) 877-0900
                                                                                         REGISTRATION NUMBER:
                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                     ASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
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l Similarity 49.6%;
67; Conservation
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South San Francisco
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                                                                                                                                                                                                                                                                             IBM PC compatible
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OF. Gateway Blvd.
                                                                                                       JEAN M.
                           877-8370
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                                                                                         32,731
                                                                           002010-005
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Pred. No. 0.29;
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nzymes, genes coding for them, isolating the genes, and methods for bleaching
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                                  Score 42.8; DB 2; Length 289;
Pred. No. 0.21;
0; Mismatches 62; Indels
                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESONDENCE ADDRESS:
ADDRESSE: Birch, Stewart, Kolasch and Birch
STREET: PO Box 747
CITY: Falls Church
STATE: VA
COUNTRY: US
ZIP: 22040-0747
COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy 41sk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPUTER: COMPUTER: OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/911,020 FILING DATE: 13-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/341,568
APTICATION NUMBER: US 08/341,568
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: MALPHY J., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 365-262P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                             1652 aaaaaaaaaaaaaaaaaaa 1673
                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08911020
                                                                                                                                                                                                                                                                                                                      252 AAAAAAAAAAAAAAAAA 273
                                  Query Match 2.6%;
Best Local Similarity 56.3%;
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penttila, Merja
Saloheimo, Anu
Marjatta, Ranua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (703) 205-800
(703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 289 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: CDNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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JS-08-911-020-3
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TITLE OF INVENTION: methods for isolating the genes, and methods for bleaching lig

TITLE OF INVENTION: pulps

NUMBER OF SEQUENCES: 7

ADDRESSPONDENCE ADDRESS:

ADDRESSEE: Birch, Stewart, Kolasch and Birch
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                                                                                                                                                                                 1539 tccacatgatggtcacacttggatataccccagtgtgggtaaggttggggtattgcaggg 1598
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                                                                                                                                                                                                                                                                  1433 TCCCCMTCCCCCCANTGNTGRAWAARAATCTGCCCCTYCCCGAAAAAAAAAAAAAAAAAA 1492
                                                                                                    2.6%; Score 43; DB 4; Length 1558;
49.6%; Pred. No. 0.29;
tive 13; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22040-u,4,
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/341,568
FILING DATE: .27-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEE: Birch, Stewart, Kolasch and Birch
: PO Box 747
Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08341568 atent No. 5661021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr, Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 365-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : Trichoderma reesei
QM9414
                                                                                                Query Match
Best Local Similarity 49.68
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 289 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                    1659 aaaaaaaaaaaaa 1673
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103..1011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
; NAME/KEY:
; LOCATION:
US-08-850-392-2
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                                                                            1532 getttggtecacatgatggteacaettggatataeeceeagtgtgggtaaggttggggtat 1591
                                                                                                                                                   132 GATTTGATGAAGAATATGACATTGCATGCCTGCTACATACGTAGATTATGATTGGGGGAG 191
                                                                                                                                                                                          Score 42.8; DB 4; Length 289;
Pred. No. 0.21;
0; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F: Barber, Glen N. INVENTION: TUMOR-CELL ASSAY METHOD AND KIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: HUMAN PKR GENE, FIGURE 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIOR APPLICATION DATA: RICH APPLICATION DATA: including application RIOR APPLICATION DATA: described below:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM compatible
SYSTEM: PC-DOS (Version 5.0)
WordPerfect (Version 5.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
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October 25, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/953,681
FILING DATE: September 29, 199.
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08/141,244
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                                                                                                                                                                                                                                1652 aaaaaaaaaaaaaaaaaaa 1673
                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08143219
Patent No. 5670330
                                                                                                                                                                                                                                                                       252 AAAAAAAAAAAAAAAAAAAA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Katze, Michael G.
Query Match 2.6%;
Best Local Similarity 56.3%;
Matches 80; Conservative
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FILING DATE: October 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
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187..1836
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Score 42.6; DB 2; Length 2628; Pred. No. 0.41; 0; Mismatches 9; Indels 0
                                           Query Match 2.5%;
Best Local Similarity 84.2%;
Matches 48; Conservative
US-08-143-219-1
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Gaps

Search completed: September 28, 1999, 16:39:36 Job time: 6962 sec

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd
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- nucleic search, using sw model OM nucleic

Run on:

2; Search time 303.81 Seconds (without alignments)
1377.741 Million cell updates/sec September 28, 1999, 16:44:42

US-09-037-657-14 1673 Title: Perfect score: Sequence:

IDENTITY_NUC Scoring table: 311585 seqs, 125096042 residues Searched:

N_Geneseq_36:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query				
2	Score	Match	Match Length DB	60	a	Description
-	1673	100.0		М	V27141	telonoment fevon
7	1614.6	96.5		~	V41688	Niche aptide segue
m	1563.4	93.4		-	V27140	NOW Description
4	1421	84.9		-	V70896	ar parpoone ANGO
S	1346	80.5		-	V27158	Incolined mutine
9	1012.2	60.5		-	V70894	THE PERFORMANCE THE PROPERTY OF THE PERFORMANCE THE PERFORMANC
7	998.2	59.7		-	V70895	a particoda ANCO
8	984.2	58.8		٠,-	V41689	Nincleof 4do segue
6	836.6	50.0		٦,	V27144	Nucleofide segue
10	830.8	49.7	834	٦,	V27143	Nicleotide segue
11	452.8	27.1		-	V27159	PGR product for
12	304	18.2	938	Н	V27142	Novel hasemond to
13	280.4	16.8	11832	-	V27148	Nincleofide section
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Description	of or one make from the state of the state o	otide	haemopoi	encoding	Unspliced murin	encodi	encodi	Nucleotide sequ	eoride s	PCR product for	haemop		eotide s	es pesse	ed s	Equine arteriti	Equine arteriti	Polydeoxyr1bonucl	OR-1 orphan rec	Human adenosine) secrete	en diseas	diseas	en diseas	en diseas	tten diseas	arren disea	atten dieses	tten diseas	atten diseas	atten diseas	atten diseas	atten d	en	atten	Batten disease	atten	n diseas	uman secrete	' fragment	9
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Length 1673; Indels

DB 1; ö

; Score 1673; I ; Pred. No. 0; 0; Mismatches

100.08;

Matches 1673; Conservative Query Match Best Local Similarity

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241 gggagcccacacagctgtaatcagcccccaggaccccaccttctcatcggctcctcct

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301 gcaagctacctgctctatacatggagacacacctggggccaccgctgaggggctctactg 360

υυ	44	45.6	2.7 11	114955		X53491 Q76213	Human adenosine Al HSV L/ST region. H
						ALIGNMENTS	
RES	RESULT	1					
V27141	141						
a .	V27141		standard; cDNA; 1673	NA; 16		BP.	
ğ	V271	V27141;					
텀	29-6	29-SEP-1998	(first	(first entry)			
Œ	Nove	Novel haemopoietin receptor	oietin	recept			
K.	Haen	Haemopoietin receptor; cell	recept	or; ce		proliferation; cell di	differentiation; cancer;
¥ 3	Ceils	cell survival; therapeutic;	I; tner	apeuti		neuronal proliteration; drug	; drug screening; ss;
SO	Mus	SD.					
H	Kev		Loc	ation/	Ona	Location/Qualifiers	
FT	CDS		i -i	11278			
FI			/*t	/*tag= a			
댪			/pr	+	H.	"Haemopoletin recentor N	NR6. 2"
PN	360M	WO9811225-A2.	•				1
G.	19-1	9-MAR-1998.					
PF	11-5	11-SEP-1997;	G02479.			-	
PR	11-5	11-SEP-1996;		246.	•		
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PA	(DZ)	(DZIE/) DZIE(DZIEGLEWSKA H E.	田田		-	
PI	Alex	tander W,	Fabri	L, Far	ley.	Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,	Υ,
M	Ko)	Kojima I, Mae	eda M,	Nash A,	z	Maeda M, Nash A, Nicola NA, Rakar S, Willson	lson T,
PI	Zhar	Zhang J;					
DR	WPI;	WPI; 98-260970/23.	70/23.				
DR	P-10	SDB; W550.	12.				
PT	New	isolated	haemop	oietin	Ä	New isolated haemopoletin receptor - used for developing produ	developing products
E.	for	modulati	ng prol	1ferat	ton	, differentiation and	survival of cells,
E.	9	neurona	l cells				
Sd	Cla	Claim 5; Page	e 84-87	; 182pi	~ å.	84-87; 182pp; English.	
ខ	The	haemopo1	etin re	ceptor	Ξ	The haemopoletin receptor (HR) NR6.2 is a form of the novel HR NR6.	the novel HR NR6.
ខ	Inte	eraction 1	between	the no	ove	1 HR and a ligand faci	litates proliferation,
ပ္ပ	diff	erentiat	ion and	Surviv	val	of a wide variety of	differentiation and survival of a wide variety of cells. The HR and it's
႘	deri	vatives	can pe	nsed fc	or 1	derivatives can be used for modulating the activity of the receptors	y of the receptors e.g.
ខ	압	egulate (develop	ment, m	mail	to regulate development, maintenance or regeneration in an array of	on in an array of
႘	diff	erent ce.	lls and	tissue	69	in vitro and in vivo.	different cells and tissues in vitro and in vivo. They can be present in
ဗ	ther	apeutics	rsed f	or mode	ula	ting neuronal prolifer	therapeutics used for modulating neuronal proliferation, differentiation
ខ្ល	and	survival	The	product	٠. د	can also be used for d	and survival. The products can also be used for detection and diagnosis,
၂ မ	0	tor can	cers or	predi	gg.	e.g. Ior cancers or predisposition to cancers, or for drug screening.	for drug screening.
מ	zedr.	sence T	673 BP;	344	Ą.	; 550 C; 474 G;	305 T;

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23-JUL-1998; U00334.
PP 15-JAN-1998; U00334.
PP 15-JAN-1998; U00334.
PP 16-JAN-1998; U00334.
PP 16-JAN-1999; US-784863.
PP 16-JAN-1999; US-784863.
PP 16-JAN-1999; US-784863.
PP 17-JAN-1999; US-784863.
PP 18-JAN-1999; US-784863.
PP 18-JAN-1999; US-784963.
PP 18-JAN-1999; US-794963.
PP 18-JAN
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1381 GGCGAGAGGTCCTGCCGGTTAAACTCTAAGGATAGGCCATCCTCCTGCTGGGTCAGACCT 1440
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V41688;
26-OCT-1998 (first entry)
Nucleotide sequence of the murine U4 gene.
Murine; U4 protein; haematopoietin receptor superfamily;
cell proliferation; immune response; antibody; cell differentiation;
autolmmune disease; cancer; allergy; ds.
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Pred. No. 0;
0; Mismatches
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122. .1399
/*tag= a
/product= "U4 proteir
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Best Local Similarity 99.1%;
Matches 1634; Conservative
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1656 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                             acatggagacacacctggggccaccgctgaggggctctactggacctcaatggtcgccg 378
                                                                                                                                                                                                                                                                                                   aatcagcccccaggaccccaccttctcatcggctcctccctgcaagctacctgctctat 318
                                                                                                                                                                                                                                                                                                                             cctgcctctgagctgtcccgcctccttaacacctccaccctggccctggcctggctaa 438
                                                                                                                                                                                                                                                                                                                                      ccttaatgggtccaggcagcagtcaggagacaatctggtgtgtcacgcccgagacggcag 498
                                                                                                                                                                                                                                                                                                                                                                          cattctggctggctcctgcctctatgttggcttgccccctgagaagccctttaacatcag 558
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                         Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 470)
Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.
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                                                                                                                                                                         Score 324.2; DB 45; Length 431;
Pred. No. 8.4e-53;
0; Mismatches 63; Indels 0;
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Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
               /lab_host="DH10B (ampicillin resistant)"
clone_lib="Soares_fetal_lung_NbHL19W"
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AI233311.1 GI:3817191
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85.2%;
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                                                                                                                                                                                  Similarity 85.2
62; Conservative
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Best Local Simil
Matches 362; C
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/db_xref="taxon:10118"
/clone="RKIDD49"
/clone=11b="Normalized rat kidney, Bento Soares"
/note="Organic kidney; Vector: pT/T3Pac; Site_1: EcoRI;
Site_2: NotI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1188 agcogcogggogggogagcccagctcgggcccggtgcggcggcgagctcaagcagttcctcg 1247
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      470 AACCGCGGGGGGGGGGAGATAGCTCGGGCCCGGTGCGGCGCGAGCTCAAGCAGTTCCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 GCAGACGGGGTGCGGCGAGAGGTCCTGCCGGCTAAACTCTGAGGATAGGCCATCCTGG
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Gene Index
Unpublished (1998)
On May 8, 1995 this sequence version replaced gi:801255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 470;
                                                                                                                The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, USA Tel: (301)-838-3529 Fax: (301)-838-0208 Email: nhlee@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 323.4; DB 43; Length
Pred. No. 1.2e-52;
0; Mismatches 41; Indels
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Best Local Similarity 87.2%;
Matches 407; Conservative
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AI333812 431 bp mRNA EST 13-FEB-1999
qp93e12.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
IMAGE:1930606 3' similar to TR:Q16354 Q16354 PROLACTIN RECEPTOR ;;
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Eutherla; Primates; Catarrhin!; Hominidae; Homo.
1 (bases 1 to 431)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
Insert Length: 1615 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 407.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                              61 CGGATCAGGAGCCCACACAGCTGTGATCAGTCCCCAGGATCCCACGCTTCTCATCGGCTC 120
                                                                                                                                                                                                                                                                                                                                                                ctcctgcaagctacctgctctatacatggagacacacctggggccaccgctgaggggct 354
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                  Score 334; DB 43; Length 4
Pred. No. 1.1e-54;
0; Mismatches 71; Indels
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/map="4pl6.1-4pter"
/clone="IMAGE:1930606"
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               20.0%;
84.1%;
            Query Match
Best Local Similarity 84.1
Matches 376; Conservative
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Unpublished (1997)
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AI333812.1
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AI333812
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/clone="lib="Soares_fetal_lung_NbHL19w"
/clone="lib="Soares_fetal_lung_NbHL19w"
/de_stage="lip weeks"
/de_stand cDNA was pite.
/de_stand cDNA was site.
/de_stand cDNA with a constructed from the same fetus as the fetal heart library, Soares fetal heart NBHI19W."
/de_stand cDNA was site.
/de_stand cDNA was cDN
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 447)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
1351 ggggatcctgccttcgggcagacggggtgcggcgagaggtcctgccggttaaactctaag 1410
                                                                                                                  1471 accatctgggcaacaaagaaacctaccagaggctggggcacaatgagctcccacaaccac 1530
                                                                                                                                                                                                                                                                                                                                                       agctttggtccacatgatggtcacacttggatataccccaqtg--tgggtaaggttgggg 1588
                                                                                                                                                                                                                                                                mRNA EST 29-OCT-1998
_lung_NbHL19W Homo sapiens cDNA clone
                                                         125 GGGGATCCTGCCCTC-GGCAGGGGGTGCGGGGGGGTCCTGCCGGCTAAACTCTAAG
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Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL
INAGE Consortium (info@inage.lini.gov) for further
Insert Length: 1667 8td Error: 0.00
Seq primer: -40mi3 fwd. ET from Amersham
High quality sequence stop: 431.
Location/Qualifiers
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Unpublished (1997)
On Aug 21, 1998 this sequence version replaced.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qe38a03.s1 Soares_fetal_lung_NDF
IMAGE:1741228 3', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1589 tattgcagggcctcccaacaatctctt 1615
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AI187074 LOCUS DEFINITION

ACCESSION

RESULT 12

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

source

FEATURES

BASE COUNT

ORIGIN

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427 GACCTICCTCCACACCACTACTCCCTCAAGTACAAGCT 465
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1 (bases 1 to 466)
NCT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1622 Std Error: 0.00 Seq primer: -400P from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             379 cctgccctctgagctgtcccgcctcataacacctccaccctggccctggccctggctaa 438
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                                  Tumor Gene Index
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2151491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 466;
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/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 354; DB 43;
Pred. No. 1.8e-58;
0; Mismatches 66;
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Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                  High quality sequence stop: 466.
                                                                                                                                                                                                                  /db_xref="taxon:9606"
/clone="IMAGE:1741879"
                                                                                                                                                                                Location/Qualifiers
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Best Local Similarity 85.6%;
Matches 393; Conservative
                                                                                                                                                                                            4. .466
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REFERENCE
AUTHORS
TITLE
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Ettheria; wetazoa; Chordata; Craniata; Vertebrata; Mammalia; Ettheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 380).

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Thelsing,B., Wplie,T., Lennon,G., Soares,B., Wilson,R., Martin,M., Moore,B., Matsing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R.
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P3NMF19.5 Mus musculus cDNA clone
                                                                                                                                                                                                                                                                                                               Unpublished (1996)
On May 9, 1995 this sequence version replaced gi:804170
                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                The Washu-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 384.
Location/Qualifiers
1. 390
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/map="3"
                                      , mRNA sequence
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W17583 390 bp
mb75b01.rl Soares mouse
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Unpublished (1997)
On Jan 19, 1998 this sequence version replaced g1:2287379.
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                    others
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                                                                                                                        Score 355.4; DB 4
Pred. No. 9.5e-59;
0; Mismatches 67
M.Fatima Bonaldo."
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Email: Robert_Strausberg@nlh.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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/db_xref="taxon:9606"
/map="839C02; 821G11; 4; 4p15.33-4p16.1; 4p15.33-4p16.1"
/clone="IMAGE:1705398"
                                                                                                                                                                            normalization to a Cot - 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."
                                                                                                                                                                                                                                                                                                                                                                                                                                              438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI185780 466 bp mRNA EST 29-OCT-1998 qe44h04.xl Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1741879 3', mRNA sequence.
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Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                             Length 466;
                                                                                                                                                                                                                                           1 others
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                                     /clone_llb="Soares_fetal_heart_NbHH19W"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                     :99
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Pred. No. 1.8e-58;
0; Mismatches 66;
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85.6%;
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Eukaryota; Metazoa;
Eutherla; Primates;
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AI394468
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//Ab_host="DH10B (ampicillin resistant)"
//Ab_host="DH10B (ampicillin resistant)"
//Ab_host="DH10B (ampicillin resistant)"
//Ab_host="DH10B (ampicillin resistant)
//Ab_host="DH10B (ampicillin resistant)
//Ab_host="DH20B (ampicillin resistant)
//A
                                                                                                                     qe50c05.xl Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
IMAGE:1742408 3' similar to TR:Q16354 Q16354 PROLACTIN RECEPTOR;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergeinh.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1552 Std Error: 0.00
Seg primer: -400P from Gibco
High quality sequence stop: 467.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 477)

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On Feb 17, 1998 this sequence version replaced g1:2150926
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Pred. No. 3.7e-60;
0; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:1742408"
/clone_lib="Soares_fetal_lung_NbHL19W"
/dev_stage="19 weeks"
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/db_xref="taxon:9606"
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AI185924.1 GI:3736562
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Matches 403; Conservative
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                                RESULT 7
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A1394468 462 bp mRNA EST 30-MAR-1999
tf79d12.xl NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2105495 3',
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187 CCTGCCCCTGAGGTCTCCCGTGTACTCAACGCCTCCACCTTGGCTCTGGCCCTGGCCAA 246
                                                                                                                           306
                                                                                                                                                                              558
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 462)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
CCAP/BTCAP) Tumor Gene Index
Unpublished (1998)
On Feb 17, 1998 this sequence version replaced gi:2887603.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                        cattotggctggctgcctgcctatgttggcttgcccctgagaagcccttaacatcag
                                                                                                                                                                                                                    307 CATCTGGCTGGCTCTGTGTTGGCCTGCCCCCAGAGAACCCGTCAACATCAG
                                                                                                                                                                                                                                                                             ctgctggtcccggaacatgaaggatctcacgtgccgctggacaccggggtgcacacggggga
                                                                                                                                                                                                                                                                                                                              367 CIGCIGGICCAAGAACAIGAAGGACIIGACCIGCGGCIGGACGCCAGGGGCCCACGGNGA
                                                            ccttaatgggtccaggcagcagtcaggagacaatctggtgtgtcacgcccgagacggcag
                                                                                                                                                                                                                                                                                                                                                                                       Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tissue Procurement: David N. Louis, M.D., Myrna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert Length: 1631 Std Error:
Seq primer: -400P from Gibco
High quality sequence stop: 454.
Location/Qualifiers
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/dev_stage="adult"

/dev_stage="adult"
/lab_nost="bH108 (Life Technologies)" with a modified
/note="vector: pT713D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I: Site_2: Eco RI: This library
consists of a mixture of individually tagged normalized
libraries constructed from rat placenta, adult lung,
brain, liver, kidney, heart, spleen, ovary, and muscle.
The tag is a string of 3-5 nucleotides present between the
Not I site and the oligo-dr track which allows
identification of the library of origin of a clone within
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NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2097265 3'
SW:IL6B_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN
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1 (bases 1 to 474)
NCI/NINDS-GAP http://www.ncbl.nlm.nlh.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP); Tumor Gene Index
Unpublished (1998)
                                                                                                                                                                                                                                      acccccacccgacgtgcacgtgagccgcgttgggggcctggaggaccagctgagtgtgc 899
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                                                                                                                                                                                         Length 428;
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Pred. No. 1.1e-65;
0; Mismatches 22; Indels
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                                                                                                                                     120 g
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                                                                                                                            mixture."
134 c 1
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94.8%;
                                                                                                                                                                                          Query Match
Best Local Similarity 94.8
Matches 405; Conservative
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tf25h01.x1 N
similar to S
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A1421423
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7, 1998 this sequence version replaced gi:3034955

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                          Robert_Strausberg@nih.gov
Procurement: David N. Louis, M.D., Myrna R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                        cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution cound through the I.M.A.G.E. Consortium/LLNL at:
                                                               Soares, Ph.
                                                                                                                                                                                                                                                                             /clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 364.2; DB 46;
Pred. No. 2e-60;
); Mismatches 69;
                                                                                                                                            www-bio.llni.gov/bbrp/image/image.html
                                                                                                                                                                       Std Error: 0.00
                                                            cDNA Library Preparation: M. Bento onaldo, Ph.D.

    474
/organism="Homo sapiens"

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                Seg primer: -40UP from Gibco
High quality sequence stop: 450.
Location/Qualifiers
                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/clone="IMAGE:2097265"
                                                                              Bonaldo, Ph.D. cDNA Library Arrayed by: Greg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.8%;
larity 85.4%;
Conservative
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405; Conserv
             Tel: (301)
Email: Robe
Tissue Proc
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                                                                                                                                   found
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Best Local Si
Matches 405;
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RESULT 4 AA039053/c LOCUS DEFINITION

ACCESSION

ORGANISM

REFERENCE

VERSION KEYWORDS SOURCE

TITLE JOURNAL COMMENT

1536

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AA866388 428 bp mRNA EST 05-FEB-1999 UI-R-A0-aj-f-04-0-UI.83 UI-R-A0 Rattus norvegicus cDNA clone UI-R-A0-aj-f-04-0-UI 3' similar to gb|AC003112|AC003112 Human DNA from chromosome 19 specific cosmid R30292, genomic sequence, complete sequence [Homo sapiens], mRNA sequence.
                                                                               acacaagacccgaaaccaggacgagggatcctgcttcgggcagacggggtgcggcgag 1386
                                                                                                                                                                                            ggcacaatgagctcccacaaccacagctttggtccacatgatggtcacacttggatatac 1566
                                                                                                                                                                                                                                                                                                        On Mar 16, 1998 this sequence version replaced g1:2961849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Jetheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 428)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="Sprague-Dawley"
/db_xref="taxon.10116"
/map="between D11S1765 and UGB"
/clone="UT-R-AO-aj-f-04-0-UI"
/clone="UT-R-AO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Res. 6 (9), 791-806 (1996)
97044477
                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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AA866388.1 GI:4230568
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Morris,M., Tan,F., Underwood,K., Moorie,B., Taleising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                             WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mousesstewarson.wustl.edu
This clone is available royalty-free through LLNL; contact the
MGI-28547
MGI-28547
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 441.
                                                                                              AA039053 445 bp mRNA EST 29-AUG-1996 m199d07.rl Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA clone IMAGE:474733 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="IMAGE:474733"
/clone_lib="Soares mouse embryo NbME13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 430.6; DB 27; Length 445; Pred. No. 4.3e-73; 0; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                   Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 .445
/organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                       The WashU-HHMI Mouse EST Project
91514788
AA039053.1 GI:1514788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="unknown"
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98.0%;
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Best Local Similarity 98.0
Matches 436; Conservative
                                                                                                                                                                                                                 Mus musculus
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14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2 ]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cgtggaggacagcgtggactggaaggtggtggatgacgtcagcaaccagacctcctgccg 1023
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                                                                                                                                                                                     Length 482;
                                                                                                                                                                                    Score 457.8; DB 26; Length
Pred. No. 2.8e-78;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
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The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                     Query Match 27.4%;
Best Local Similarity 99.4%;
Matches 470; Conservative
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AA049278.1
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AUTHORS
                                                                                                                        COUNT
                                                                                                                                                                                                                                                                                                                                                                                              785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 29; Length 503;
               MO 63108
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through )
MAGE Consortium (info@image.llnl.gov) for fu
MG1289790
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Pred. No. 1.1e-76;
0; Mismatches 6;
                                                                                                                     Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 486. Location/Qualiflers 1.503
                                                                                                                                                                                /organism="Mus musculus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.9%;
98.0%;
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Best Local Similarity 98.0
Matches 497; Conservative
                             Tel: 314 286 1800
Fax: 314 286 1810
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W66776.1 GI:1375694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     house mouse.
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AUTHORS
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Thelsing, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:289787
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                             house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                   Unpublished (1996)
On Dec 30, 1996 this sequence version replaced gi:1528951
                                                                                                                                                                                                                                                  Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH108"
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100.0%; Pred. No. 1.9e-79;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 437. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                      The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                               mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="IMAGE:479043"
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AA049280.1 GI:1755311
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Best Local Similarity 100.
Matches 464; Conservative
                                                                                                                                                                         Waterston, R.
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Email:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 482)
Marra, M. Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Thelsing, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
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This clone is available royalty-free through LLNL; contact the
INMGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                  301 ACGIGAGCCGCGIIGGGGCCIGGAGGACCAGCIGAGIGIGCGCIGGGICICACCACCAG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W66776. 482 bp mRNA EST 14-JUN-1996 me17bl1.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:387741 5' similar to PIR:B38252 B38252 granulocyte colony-stimulating factor receptor precursor ;, mRNA sequence.
                        917
                                                                                                                                                                                                                 7.76
                                                                                                                                                                                                         ctctcaaggatttcctcttccaagccaagtaccagatccgctaccgcgtggaggacagcg
                                                                                                                                                                                                                                    acgtgagccgcgttgggggcctggaggaccagctgagtgtgcgctgggtctcaccaccag
ctgatgteeteacactggatgteetggacgtggtgaceacggaceeceacegacgtge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of MedicineP
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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/sex="unknown"
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Possible reversed clone: similarity on wrong strand
                                                                                                                                                                                                                                                                                                           /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
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The WashU-HHMI Mouse EST Project
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Location/Qualifiers
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/db_xref="taxon:10090"
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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

September 28, 1999, 15:38:03; Search time 2095.87 Seconds (without alignments) 1574.548 Million cell updates/sec

Run on:

US-09-037-657-14 1673

1 ggcacgagettcgetgtccg.....aaaaaaaaaaaaaaaaaaa 1673 IDENTITY_NUC Title: Perfect score: Sequence: Scoring table:

2546578 segs, 986266752 residues

Searched:

Database :

em_est18

db_est2 gb_est2

em_est20 em_est21

em_est22:*
em_est23:*
em_est24:*
em_est25:*
em_est25:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	9280	75 mel/bll.	3 m199d07	56388 UI-R-A	21423 tf25h0	35924 qe50c0	34468 tr79dl	1002 gb69g04	.85/80 qe44n04	263 MD/3D01.II	23812 4636303	33311 EST229	71408 UI-R-C2-	269388 q126b05.	379568 UI-R-GO-	574687 UI-R-GO-	570108 we65£03	042914 zk56f01.	32198 AV032198	2/0365 Vab3n12.	575060 UI-R-GU	143001 ZK351011.	7407 vm88d09 s	10798 AV01079	11309 AV01130	74921 oy04d08	25924 UI-R-A1-	77893 EST9055	009 EST00035	5/5 ZDI/IDS.51	33008 OI-K-C3	22120 OM43612.	2/094 ZK69C11.	1537 0876	74006	14965 mh23e02.	64328 q109c05.	17616 tq80c02.	57868 qv13b02.	205 mc69e09.	49564 EST1923
	AAO	W66776	AA049	AA86638	AI42142	AI18592	AI39446	A116100	A1185/8	W1/086	A122201	AT233	AI07140	AI26938	AI57956	AI57468	A167010	AA04291	AV03219	AA27036	AI57506	AA04300	78740	AV01079	AV011	AI07492	AA92592	AA37789	H1400	N/88/8	ALSSSOD	AASZZZZ	AA12/09	5215164	AT374	AA01496	AI26432	AI41761	AI35786	W4220	.AA849
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ALIGNMENTS

RESULT 1
AAO49280
LOCUS
DEFINITION

AA049280 464 bp mRNA EST 30-DEC-1996 mj45d02.rl Soares mouse embryo NDME13.5 14.5 Mus musculus cDNA clone IMAGE.479043 5' similar to SW:ILGB_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR; mRNA sequence. AA049280 g1755311

ACCESSION NID

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Email: insourceseblue.weeg.ulowa.edu

The sequence tag present in the CDNA between the NotI site and the oligo-dr track served to identify it as a clone from the normalized adult Lung library. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C2 library, which is a subtracted library derived from the UI-R-C1 library, which is a subtracted library derived from the UI-R-C0 library, which is a subtracted library consisted of an axture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day between the Not I site and the oligo-df track which allows identification of the library of origin of a clone within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the ULT-C.2. library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the mixture. The subtracted library (UT-R-C2) was constructed as follows: PCR amplified cDNA inserts from UT-R-C1 clones from which 3' ESTs had been derived was
                                                          Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                   451; pčksteln Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319.335 9565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used as a driver in a hybridization with the UI-R-C1
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
1 (bases 1 to 464)
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note="Vector: pr7r3D-Pac (Pharmacia) with a modi
olylinker; Site_1: Not I; Site_2: Eco RI; The UI
                                                                                                                                                                                                                          On Sep 12, 1996 this sequence version replaced gi:1404537
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Pred. No. 9.1e-52;
); Mismatches 42; Indels
                                                                                                                                                                                                                                                                                     Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref="taxon:10116"
clone="UI-R-C2-nb-d-08-0-UI"
clone_lib="UI-R-C2"
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Best Local Similarity 86.9%;
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                                                             AUTHORS
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                                          1447 tcacctgaattggagccctctgtac----catctgggcaacaaagaaacctaccagag
                                                                                gotgggggaaatgagctcccacaaccacagctttggtccacatgatggtcacacttgga
                                                                                                                                                              163 GCTGGGGCACAATGAGCTCCCACAACCACAGCTTTGG-CCACATGATGGTCAACTTTGGA
283 GGTCCTGCCGGCTAAACTCTGAGGATAGGCCATCCTCCTGCTGGATGCAGACCTGGAGGC
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Search completed: September 28, 1999, 15:38:09 Job time: 3277 sec

A70384 Sequence 14 A70394 Sequence 24 AF059293 Homo sapi AC003112 Human DNA Y07862 Plasmid pEA

Sequence 22 Sequence 28 Sequence 38 Sequence 12

A70408

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Database Searched:

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AJ000937 Oryzias I
U75932 Rattus norv
AF106697 Homo sapi
X79204 H.sapiens S
S83440 RNH-1-prepr
Y14040 Homo sapien
AF047611 Euroglyph
E0221 conv encodi
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X1811 O.sativa mR
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Patent: WO 9811225-A 19-MAR-1998;
NICOLA NICOS ANTONY (AU)
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Nicola,N.A., Fabri,D., Farley,A., Nash,A., Willson,T., Rakar,S.,
Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
Kikuchi,Y.
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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd
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Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,
Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
Kikuchi,Y.
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1 Similarity 100.0%; Pred. No. 9.1e-158;
888; Conservative 0; Mismatches 0;
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                    tgoetccaeccetegaagtgagegecegggecegggeggg 138
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16.3%; Pred. No. 8.1e-130;
.ve 0; Mismatches 27; Indels 3;
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ef="taxon:32644"
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/db_xref="taxon:32644"
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Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
Kikuchi,Y.
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                                                                                                                                                          Db 11283 CAACACCGCACTCTTCTTTCCAAGCACGAGGGGATCCTGCCCTCGGGCAGGGG 11342
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                                                                                                                                                                                                                                                                                                                                  cacttggatataccccagtgtgggtaaggttgggggtattgcagggctcccaacaatctc
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                  11043 GTGTGCGAGCCGCGGGGGGGGGGGGCGAGCTCGGGCCGGTGCGGCGCGAGCTAG
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   gtgtgcgagccgcgggggggggggccagctcgggcccggtgcgggcgcgagctcaagcag
                                               tteeteggetggeteaagaageacgeatactgetegaacettagttteegeetgtaegae
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Sequence 12 from Patent WO9811225.
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Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,
Shang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
Kikuchi,Y.
                                                                                                                                              1 ggcaccgtttacttcgtccaagtgcgttgtaacccattcgggatctatgggtcgaaaaag
                                                                                                                                                                                                                                                                                             cggcgcgagctcaagcagttcctcggctggctcaagaagcacgcatactgctcgaacctt
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Best Local Similarity 100.0%; Pred. No. 3.8e-48;
Matches, 304; Conservative 0; Mismatches 0;
32.5%; Score 305; DB 5; 100.0%; Pred. No. 2.5e-48; ive 0; Mismatches 0;
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/db_xref="taxon:32644"
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14 from Patent
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                    Similarity 100.
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A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME PALENT: WO 9811225-A 19-MAR-1998;
NICOLA NICOS ANTONY (AU)
., Farley, A., Nash, A., Willson, T., Rakar, S.,
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                                                                                                                                                                                                                                                         Shang, J., Alexander, W., Hilton, D.J., Kojima, T., Maeda, M. and
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'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.6%; Score 249.8; DB 5 ilarity 86.8%; Pred. No. 5.7e-38; Conservative 0; Mismatches 42
                                                                                                                                                             1391 bp DNA
24 from Patent WO9811225.
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Nicola, N.A., Fabri, L
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/note="similar to cytokine type-1 receptor family members; similar to the sequence presented in GenBank Accession Number ACO03112"
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YEDSVDWRVVTVDDVSRQTSCRLAGLKRGTVTFVQVRCNPFGIYGSKAGIWSEWSHPT
AASTPRSERPGGGGACEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWR
AWQKSHKTRNQDGGILPSGRRGTARGPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (14-APR-1998) Dept. of Immunology, Serono Pharmaceutical
Research Institute, 14, Chemin des Aulx, Plan-les-Ouates, GE 1228,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1116)
Elson, G.C.A., Graber, P., Losberger, P., Herren, S., Gretener, D., Menoud, L.N., Wells, T.N.C., Kosco-Vilbois, M. H. and Gauchat, J.F. CLF.1, a Novel Soluble Protein Shares Homology With Members of J. Immunol. (1999) In press

Closes 1 to 1716)
Elson, G.C.A., Graber, P., Losberger, P., Herren, S., Gretener, D., Menoud, L.N., Wells, T.N.C., Kosco-Vilbois, M.H. and Gauchat, J.F. Direct Submission
                                862 CGGCGCGAGCTCAAGCAGTTCCTGGGCTGGCTCAAGAAGCACGCGTACTCCTCCAACCTC 921
                                                                                                                                             02-AUG-1998
cggcgcgagctcaagcagttcctcggctggctcaagaagcacgcatactgctcgaacctt
                                                                                                       241 agtitccgcctgtacgaccagtggcgtgcttggatgcagaagtcacagagacccgaaac
                                                                                                                                                                                                                                                                                                                                                                                         AFUS9293 1716 bp MRNA PRI 02-AUG-19
Homo sapiens cytokine-like factor-l precursor (CLF-1) MRNA,
AFOS9293
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/profein_d=AAC8335.1"
/db_xref="PDi:3372627"
/db_xref="GI:3372627"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="putative"
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AF059293.1 GI:3372626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119. .1387
/gene="CLF-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="CLF-1"
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                                                                                                                                                                                                                    301 caggtaggaaagttggg 317
                                                                                                                                                                                                                                                                               982 CAGCACAGGACGAGGGG 998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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Query Match Best Local Simil Matches 270; C

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frame: 1, quality: excellent, score: 100.000--DDS similarity to AA047548 zf15e02.r. Scores fetal heart NbHH19W Home sapiens cDNA clone 377018 5' (139. .221); 100% identity. --DDS similarity to AA136115 zk90b04.rl Scores pregnant uterus NbH9W Home sapiens cDNA clone 490063 5' (111. .192); 99% identity.--DDS similarity to AA432628 zx33f04.rl Scores total fetus Nb2HF8 9W Home sapiens cDNA clone 500 zx33f04.rl Scores total fetus Nb2HF8 9W Home sapiens cDNA clone 500 zx33f04.rl Scores total fetus Nb2HF8 9W Home sapiens cDNA clone 365523 5' (62. .144); 100% identity.--DDS similarity to AA009412 zc82h02.rl Scores fetal heart NbHH19W Home sapiens cDNA clone 365523 5' (62. .144); 100% identity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Juliary. Lissal force and solution of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 heart NbH19W Homo sapiens CDNA clone 377018 5' (1. 138): 96% identity. --Other overlapping matches: (10435. 1048) DbS similarity to AA136115 zk90b04.rl Scares pregnant uterus NbHPU Homo sapiens cDNA clone 490063 5' (1. 110); 93% identity. --(10466. 10548) DDS similarity to AA455628 zx33304.rl Scares total fetus Nb2HPS 9W Homo sapiens CDNA clone 788287 5' (1. 82); 95% identity. --(10486. 10548) DDS similarity to AA0455628 similarity to AA0455628 similarity to AA0455628 clone 788287 5' (1. 82); 95% identity. --(10486. 10548) DDS similarity to AA009412 ze82h02.rl Scares fetal heart NbHH19W Homo sapiens CDNA clone 365523 5' (1. 61); 97%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           frame: 1, quality: good, score: 63.000"
complement(9629. 9672)
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frame: 1, quality: excellent, score: 75.000"
complement(9928. 10123)
/rpt_family="Alu"
10409. 10548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          grail2exons_human_1.3,
63.000"
                        grail2exons_human_1.3,
71.000"
                                                                                                                         gra112exons_human_1.3,
62.000"
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                                                                                                                                                                                                                           /standard_name="endogenous retroviral sequence"
                                                                                                                                                                                                                                                              /note="HERV9 retroviral sequence"
complement(3269. .3544)
                                                       frame: 1, quality: good, score:
complement(1383. .1444)
/note="predicted exon, program:
                                                                                                                                                            rame: 1, quality: good, score:
257. .8516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(11869, .12161)
/rpt_family="Alu"
12502, .12581
                                                                                                                                                                                                                                                                               /rpt_family="Alu"
5425, .5722
                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="Alu"
complement(7505, 770)
/rpt family="Alu"
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complement(9445. .9505)
/note="predicted exon, ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="Alu"
9358. .9535
                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="Alu"
complement(6486.
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/cell_line="5HL2-B"
/cell_line="5HL2-B"
/clone_lib="LL19NC03 R chromosome 19 cosmid library"
/note="LL19NC03 cosmid library constructed at LLNL from
flow-sorted chromosomes from hybrid 5HL2-B, which carries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lamerdin, J.E.
Direct Submission
Submitted (21-NOV-1997) Human Genome Center, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
Location/Qualifiers
1. 40668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1208 cesceceaecreaacaerrecresecresercaasaascaceseracrecreaecre 1267
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                                                                                                                                                                                                                                                                                                                                1028 GGCACCGIGTACTICGIGCAAGIGCGCIGCAACCCCTITGGCAICTAIGGCICCAAGAAA 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cggcgcgagctcaagcagttcctcggctggctcaagaagcacgcatactgctcgaacctt 240
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                                                                                                                                                                                                                                                                                                                                                                                                      gogggaatctggagogagtggagocacccaccgctgcctccaccctcgaagtgagogc 120
                                                                                                                                                                                                                                                                 ggcaccgtttacttcgtccaagtgcgttgtaacccattcgggatctatgggtcgaaaag 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40668 bp DNA PRI 21-NOV-1995.
from chromosome 19 specific cosmid R30292, genomic complete sequence.
                                                                                                                                    DB 11; Length 1716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome 19 as its only human chromosome
                                                                                                                                                                                               34; Indels
                                                                                                                                Score 249.6; DB 1:
Pred. No. 6.2e-38;
0; Mismatches 34.
   273
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/db_xref="taxon:9606"
/clone="R30292"
/chromosome="19"
      ρ
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      525
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                                                                                                                                    26.6%;
      U
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      623
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                                                                                                                                                                   Similarity
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AC003112
      ø
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RESULT 9 AC003112/c LOCUS DEFINITION

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9 ò ORGANISM

VERSION KEYWORDS SOURCE

REFERENCE AUTHORS

REFERENCE AUTHORS TITLE JOURNAL

FEATURES

JOURNAL

TITLE

ACCESSION NID

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Comprement(127) 0. .14029

frame: 2, quality; good, score: 61.000--Other overlapping matches: -(1376. .13826) DDS similarity to Anology12 ce82h02.r1 Scares fetal heart NbHHJ9W Home sapiens cDNA clone 35523 5' (428. 496); 97% identity. -(13756. .13984) DDS similarity to Anology3 ze82h02.s1 Scores fetal heart NbHHJ9W Home sapiens cDNA clone 365523 3' (227. 1); 98% identity. --(13756. .13984) DDS similarity to And Solos zeach fetal heart NbHHJ9W Home sapiens cDNA clone 365523 3' (227. 1); 98% identity. --(13756. .13984) DDS similarity to And Solos zeach fetus Nb2HF8 9W Home sapiens cDNA clone 788287 3' (228. .1); 99% identity. --(13756. .13984) DDS similarity to And 14885. .15317

//note="DDS similarity to And 16406 zvlle07.s1 Scares NhHMPu sapiens cDNA clone 302666 5' (11. .355); 94% identity. 431/433 (99%). ---(14884. .1537) DDS similarity sapiens cDNA clone 302666 5' (11. .355); 94% identity. -(1527. .14885) DDS similarity to And 12769 zk89cll.s1 Scares pregnant uterus NbHPU Home sapiens cDNA clone 302666 5' (11. .355); 94% identity. --(1527. .14885) DDS similarity to W46603 ccashio.r1 Scares pregnant uterus NbHPU Home sapiens cDNA clone 302666 5' (11. .355); 94% identity. --(1527. .14885) DDS similarity to W46603 ccashio.r1 Scares pregnant uterus NbHPU Home sapiens cDNA clone 32467 5' (228. .1); 98% identity. --(1527. .14887) DDS similarity to W46604 cc32hl0.r1 Scares senescent fibroblasts NbHSF Home sapiens cDNA clone 32467 3' (328. .1); 98% identity. --(1527. .1688) DDS similarity to W46604 cc32hl0.s1 Scares senescent fibroblasts NbHSF Home sapiens cDNA clone 32467 3' (322. .465); 96% identity. --(1527. .15688) DDS similarity to W46604 cc32hl0.s1 Scares senescent fibroblasts NbHSF Home sapiens cDNA clone 32467 3' (322. .465); 96% identity. --(1527. .15688) DDS similarity to W46604 cc32hl0.s1 Scares senescent fibroblasts NbHSF Home sapiens cDNA clone 32467 3' (322. .465); 96% identity. --(1527. .15688) DDS similarity consent fibroblasts NbHSF Home sapiens cDNA clone 32467 3' (322. .465); 96% identity. --(1527
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/note-"DDS similarity to AA121532 zk89c11.s1 Soares
pregnant uterus NbHPU Homo sapiens cDNA clone 490004 3'
(389. 343); 99% identity.-DDS similarity to AA127694
zk89c11.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490004 5' (77. 125); 90% identity.-(15735. 15713)
DDS similarity to W46603 zc32hl0.r1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 324067 5' (351. 329); 100% identity.--(15735. 15713) DDS similarity to W46604 zc32hl0.s1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 324067 3' (299. 321); 100%
pregnant uterus NDHPU Homo sapiens cDNA clone 490063 5/ (395. 477); 92% identity. --DDS similarity to AA009412 ze82h02.r1 Soares fetal heart NDH19W Homo sapiens cDNA clone 36523 3 (347. 427); 94% identity. --DDS similarity to AA009693 ze82h02.s1 Soares fetal heart NDH19W Homo sapiens cDNA clone 365523 3 (306. 228); 99% identity. --DDS similarity to AA450010 zx33f04.s1 Soares total fetus ND2HF8 9w Homo sapiens cDNA clone 788287 3 (509. 229); 99% identity. --

Complement(1296. 13240)
                                                                                                                                      similarity
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/rpt_family="Alu"
complement(13756. .14029)
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JUNESS. 1 GI:1835169
YO7862.1 GI:1835169
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YOFFI ORFIA: ORFIA: ORFIA: Teplicase: replicase
POLYPROTEIN: Thosomal frameshift signal.
ESM Territis virus:
ESM FQUINE arteritis virus:
Viruses: SSRNA positive-strand viruses, no DNA stage; Nidovirales;
Arteriviridae; Arterivirus.
TE (bases 1 to 15528)
SSR Van Dinten, L.C. den Boon, J.A., Wassenaar, A.L., Spaan, W.J. and
SRIJGEY, E.J.
An infectious arterivirus cDNA clone: identification of a replicase
                                                                                  Complement(184.0. .18697)

// note="predicted exon, program: grail2exons_human_1.3, frame: 1; quality: excellent, score: 100.000--DDS
slmilarity to W66776 me17bll.r1 Soares mouse embryo
NbMEl3.5 14.5 Mus musculus cDNA clone 387741 5' similar to
PIR:B38252 B38252 granulocyte colony stimulating factor receptor precursor (316. .158); 92% identity.--DDS
slmilarity to AA049280 mj45602.r1 Soares mouse embryo
NbMEl3.5 14.5 Mus musculus cDNA clone 479043 5' similar to
SW:IL6B_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN
PRECURSOR (274. .431); 93% identity.--"
(157. .1); 82% identity. --(18438. .18406) DDS similarity to | AAO49280 mj45d02.r1 Soares mouse embryo NDME13.5 14.5 Mus musculus cDNA clone 479043 5' similar to SW:ILGE_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA PRECURSOSR (432. .464);
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Plasmid pEAV030 containing cDNA of Equine arteritis virus, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15973 GTACTGCTCCAACCTCCAGCTCTACGACCAGTGGCGAGCCTGGATGCAGAAGTC 15914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15913 GCACAAGACCCGCAACCAGGTAGGAAGGAGGACCCTCGGGCGTGGGGGTGGGGACAGGG 15854
                                                                                                                                                                                                                                                                                                                                                                                                  429
                                                                                                                                                                                                                                                                                                                                                                                                                                                         atactgetcgaacettagtttccgcctgtacgaccagtggcgtgcttggatgcagaagtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                430 gcagacggggtgcgggcgagggtaagggggtctgggtgagtggggcctacagcagtctag
                                                                                                                                                                                                                                                                                                                                                   Indels 35;
                                                                                                                                                                                                                                                                                                                   Length 40668;
                                                                                                                                                                                                                                                                                                               Score 218; DB 11;
Pred. No. 4.3e-32;
0; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  285 acacaagacccgaaaccaggtaggaaag------
                                                                                                                                                                                                                                                                                                             Score 218;
                                                    000560 INTERL
88% identity.
                                                                                                                                                                                                                                                                                                           23.28;
                                                                                                                                                                                                                                                                                                                          Similarity 72.4%;
14; Conservative
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                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                          Best Local Sim
Matches 314;
                                                                                                                                                                                                                                                                                                             Query Match
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VERSION
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source

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COMMENT FEATURES

REFERENCE AUTHORS TITLE JOURNAL

JOURNAL MEDLINE source

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CDS

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VWTRINEVVVLTASHVVGRANMATLKIGDAMLTLTFKKNGDFAEAVTTQSELPGNWPQ
LHFAQPTTGPASWCTATGDEEGLLSGEVCLAWTTSGDSGSAVVQGDAVVGVHTGSNTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVAYVTTPSGKLLGADTVTLSSLSKHFTGPLTSIPKDIPDNIIADVDAVPRSLAMLID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIMRGSPORAWHITTRSCKLKSYYVCDISEADWSCLPAGNYGGYNPPGDGACGYRCLA
FWNGAIVVSAGCSSDLWCDDELAYRVFQLSPTFTVTIPGGRVCPNAKYAMICDKQHWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPLASAGVASDSAPKWRVAKTVYSSAERFRTELVQRARSVGDVLVQALPLKTPAVORT
TWTLKMMRSRFSWHCDVWYPLAVIACLLPIWPSLALLLSFAIGLIPSVGNNVVLTALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDHFSKPTIDVVGMATGWSGCYTGTAAMERQCASTVDPHSFDQKKAGATVYLTPPVNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLVCHRLAISALDLLTLASPLVLLVFPWASVGLLLACSLAGAAVKIQLLATLFVNLFF
PQATLVTMGYWACVAALAVYSLMGLRVKVNVPMCVTPAHFLLLARSAGGSREQMLRVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAPTNSLLGVARDCYVTGTTRLYIPKEGGMVFEGLFRSPKARGNVGFVAGSSYGTGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVYQFPGWAIGTVLAVCSITMLAAALGHTLLLDVFSASGRFDRTFMMKYFLEGGVKES
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                                                                                                                                               Snijder, E.J.
Direct Submission
Submitted (10-SEP-1996) E.J. Snijder, Dept. of Virology, Institute
of Medical Microbiology, Leiden University, AZL Building 1, Room
P4-26, Postbus 9600, 2300 RC Leiden, NETHERLANDS
Related sequences: X53459, X52275, X52276, X52277 & A02710.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation-"MATFSATGFGGSFVRDWSLDLPDACEHGAGLCCEVDGSTLCAEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGFCWLKLLPPDRREAGLRLYYNHYREQRTGWLSKTGLRLWLGDLGLGINASSGGLKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRPVPAPRVRPSANSSGDVKDPAPVPPVPKPRTKLATPNPTQAPIPAPRTRLQGASTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSSANYVASMDHQCEGAACLALLEEEHYYRAVRWRPITGALSLVLNLLGQVGYVARST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LCCLFTPLSMRLCLFHLVCATVTGNVISLWFYITAAGTSYLSEMWFGGYPTMLFVPRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RVVDARLAIEEASVFISTDHASAKRFPGARFALIPVYANAWVVSPAANSLIVTTDQEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u> 2yrnilnaslovdrdaarsrrlmakladfaveqevtagdrvvvidgldrmahfkddl</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(225. .5405,5405. .9751)
note="ORFlab; slippery sequence causes -1 frameshift"
point mutation that abolishes discontinuous mRNA transcription
Proc. Natl. Acad. Sci. U.S.A. 94 (3), 991-996 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Organism-"Plasmid pEAV030"

(db_xref-"taxon:57026"

(lab_host-"Escerichia coli strain K12-PC2495"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. 15528
/organism-"Plasmid pEAV030"
/db xref="taxon:57026"
/lab_host="Escerichia coli strain K12-PC2495"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'product-"replicase ORF1a polyprotein"
'protein_id-"CAA69186.1"
'db_xref-"PID:e280813"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Equine arteritis virus"
/db_xref="taxon:11047"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'organism="Cloning vector pUC18"
|db_xref="taxon:72227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'db_xref="SPTREMBL:P89938"
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/db_xref="PID:e280872"
/db_xref="PID:q1835171"
/db_xref="GI:1835171"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref-"PID:g1835170"
                                                                                                                                                                                                                                                                                                                                                                                             .ocation/Qualifiers
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/note="ORF1a"
                                                                                                              (bases 1 to 15528)
                                                         97175715
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FDHLESSSYAPFINAYRQAILSQYPQELQLEAINCKLLAVVAPALYHNYHLANLTGPA TWVVPTVGQLHYYASSSIFASSVEVLAAIILLFACIPLVTRVYISFTRLMSPSRRTSS EPLASAGVASDSAPKWRVAKTVYSSAERFRTELVQRARSVGDVLVQALPLKTPAVORY TMTLKMMRSRFSWHCDVWYPLAVIACLLPIWPSLALLLSFAIGLIPSVGNNVVLTALL translation-"MORFSFSCYLHWLLLLCFFSGSLLPSAAAWRGVHEVRVTDLFK HIMRGSPQRAWHITTRSCKLKSYYVCDISEADWSCLPAGNYGGYNPPGDGACGYRCLA FMNGATVVSAGCSSDLWCDDELAYRVFQLSPTFTVTIPGGRVCPNAKYAMICDKQHWR PRPVPAPRVRPSANSSGDVKDPAPVPPVPKPRTKLATPNPTQAPIPAPRTRLQGASTQ VSSANYVASMDHOCEGAACLALLEEEHYYRAVRWRPITGALSLVLNLLGQVGYVARST **FDAAYVPCTVFDLCSFAILYLCRNRCWRCFGRCVRVGPATHVLGSTGQRVSKLALIDL** <u> DHFSKPTIDVVGMATGWSGCYTGTAAMERQCASTVDPHSFDQKKAGATVYLTPPVNS</u> GSALQCLNVMWKRPIGSTVLGEQTGAVVTAVKSISFSPPCCVSTTLPTRPGVTVVDHA LLVCHRLAISALDLLTLASPLVLLVFPWASVGLLLACSLAGAAVKIQLLATLFVNLFF PQATLVTMGYWACVAALAVYSLMGLRVKVNVPMCVTPAHFLLLÄRSAGQSREQMLRVS AAAPTNSLLGVARDCYVTGTTRLYIPKEGGMVFEGLFRSPKARGNVGFVAGSSYGTGS VWTRNNEVVVLTASHVVGRANMATLKIGDAMLTLTFKKNGDFAEAVTTQSELPGNWPQ **LHFAQPTTGPASWCTATGDEEGLLSGEVCLAWTTSGDSGSAVVQGDAVVGVHTGSNTS** SVAYVTTPSGKLLGADTVTLSSLSKHFTGPLTSIPKDIPDNIIADVDAVPRSLAMLIC **GLSNRESSLSGPQLLLIACFMWSYLNQPAYLPYVLGFFAANFFLPKSVGRPVVTGLL**K LCCLFTPLSMRLČLFHLVCATVTGNVISLWFYITAAGTSYLSEMWFGGYPTMLFVPRF LVYQFPGWAIGTVLAVCSITMLAAALGHTLLLDVFSASGRFDRTFMMKYFLBGGVKES VTASVTRAYGKPITQESLTATLAALTDDDFQFLSDVLDCRAVRSAMNLRAALTSFQV LVPLTTKVVGGSRCTICDVVKEEANDTPVKPMPSRRRRKGLPKGAQLEWDRHQEEKRN AGDDDFAVSNDYVKRVPKYWDPSDTRGTTVKIAGTTYQKVVDYSGNVHYVEHQEDLLD ILLGYVRACPGYWFIFRRTHRSLIDAYWDSMECVYALPTISDFDVSPGDVAVTGERWD **IAPAAETALCGDLEKYNLSTQGFVLPSVFSMVRAYLKEEIGDAPPLYLPSTVPSKNS** OAGINGAEFPTKSLOSYCLIDDMVSOSMKSNLQTATMATCKROYCSKYKIRSILGTNN CTMCEGSPKOMVPKVPHPILDHLLCHIDYGSKEELTLVVADGRTTSPPGRYKVGHKV AVVADVGGNIVFGCGPGSHIAVPLQDTLKGVVVNKALKNAAASEYVEGPPGSGKTFHI LPQVGTSEGETFVDEVAYFSPVDLARILTQGRVKGYGDLNQLGCVGPASVPRNLWLRI FVSLEPLRVCHRFGAAVCDLIKGIYPYYEPAPHTTKVVFVPNPDFEKGVVITAYHKDI **GLCHRTIDSIQGCTFPVVTLRLPTPQSLTRPRAVVAVTRASQELYIYDPFDQLSGLL**F FTKEAEAQDLIHGPPTACHLGQEIDLWSNEGLEYYKEVNLLYTHVPIKDGVIHSYPN(GPACGWEKQSNKISCLPRVAQNLGYHYSPDLPGFCPIPKELAEHWPVVSNDRYPNCL(nsrafldeaeekfaaahphaclgeinkstvggshfifsqylppllpadavalvgasla GKAAKAACSVVDVYAPSFEPYLHPETLSRVYKIMIDFKPCRLMVWRNATFYVQEGVD/ SIGAYAAEWALSTEPPP DLQCDNLRAKDAFPSLGYALSIGQSRLSYMLQDWLLAAHRKEVMPSNIMPMPGLTPDC RVVDARLA I EEASVFISTDHASAKRFPGARFALTPVYANAWVVSPAANSLI VTTDQEQ LLPPDRREAGLRLYYNHYREQRTGWLSKTGLRLWLGDLGLGINASSGGLKF LYNRLTASGVDPALLRVGQGDFLKLNPGFRLIGGWIYGICYFVLVVVSTFTCLPIKCG <u>OYRNILNASLQVDRDAARSRRLMAKLADFAVEQEVTAGDRVVVIDGLDRMAHFKDDLV</u> IGLGLRACLSGVTAAFQKAGKDGSPIYLGKSKFDPIPAPDKYCLETDLESCDRSTP /SLVLYTQHMLLCGLEGYFPEIAEKYLDGSLELRDMFKYVRVYIYSDDVVLTTPNOH // CHIGAKNPSEYYEAAVSIFKDSIICCDEDWWTDLHRRISGAARTDGVEFPTIEMLTS! /KDVLAVVGSATLVVPTHASMLDCINKLKQAGADPYFVVPKYTVLDFPRPGSGNITV! ITLQQVCELSKPCSAGYMVGQSVFVQTPGVTSYWLJEWVDGKARALPDSLFSSGRFE: SVPTNALEATACYRAGCEAVTDGTNVIATIGPFPEQQPIPDIPKSVLDNCADISCD RTKQYESAVCTVCGAAPVAKSACGGWFCGNCVPYHAGHCHTTSLFANCGHDIMYRST' GYAIVRRYIVKRLLSSTEVFLCRRGVVSSTSVQTICALEGCKPLFNFLQIGSVIGPV YVLGKGSYEGLDQDKVLDLTNMLKVDPTELSSKDKAKARHVAHLLLDLANPVEAVNQ FESPGGGRAKRLTADLVHAFQGFHGASYSYDDKVAAAVSGDPYRSDGVLYNTRWGNI LVRWFAINLIFELAGQPELVHSYVLNCCHDLVVAGSVAFTKRGGLSSGDPITSISNI IGTRDPFCRRVFSVPVTKTOEHCHAGMCASAEGISLDSLGLTQLQSYWIAAVTSGLV nlraphifpgdvgrrtfadskdkgfvalhsrtmflaardflfnikfvcdeeftktp1 AASFDRWVPHLOALLGFKVDPKKTVNTSSPSFLGCRFKQVDGKCYLASLQDRVTRS 5399, .5405 /note-"ribosomal frameshift slippery sequence' 9824, .10507 'product="small glycoprotein" PID:e265651 TSALAAVSKLIKVPANEP db_xref="G1:183517 . .10507 /gene="Gs" 9824. .105 dp_xref-/gene="Gs rotein_

GTLPRRKIL

misc_feature

gene

CDS

us-09-037-657-16.rge

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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Sciuropnathi; Muridae; Murinae; Rattus.
1 (bases 1 to 1934)
Enmark,E. and Gustafsson,J.A.
Enmark,E. and Gustafsson,J.A.
Oril ON ORPHAN RECEPPOR BELONGING TO THE NUCLEAR RECEPTOR FAMILY
PATENT: WO 9605300-A 1 22-FEB-1996;
KAROBIO AB (SE)
Other publication AU 3384495 960307.
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Baud,V., Mears,A.J., Lamour,V., Scamps,C., Duncan,A.M.,
McDermid,H.E. and Liptinskl,M.
The E subunit of vacuolar H(+)-ATPase localizes close to the
contromere on human chromosome 22
Hum. Mol. Genet. 3 (2), 335-339 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.1%; Score 67; DB 10; Length 1319; Best Local Similarity 83.5%; Pred. No. 0.0012; Matches 76; Conservative 0; Mismatches 15; Indels
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    1934
/organism="Rattus norvegicus"

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                                                                                                                                            Location/Qualifiers
1. 1319
Cyrganism="Homo sapiens"
Ab_Xref="taxon:9606"
/chromosome="22q11"
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Sequence 1 from Patent W09605300.
A49139
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/db_xref="taxon:10116"
                                                                                                                                                                                                                                                /tissue_type="Ewing tu
/cell_line="IARC-EWI1"
/clone="61EW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 g
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                                                                                                                                                   FYAANVTFPSHFORHFAAAODFVVHTGXEYAGVTMLVHLFANLVLTFPSLVNCSRPVN
VFANASCVQVVCSHTNSTTGLGQLSFSFVDEDLRLHIRPTLICWFALLLVHFLPMPRC
                                                                                                                                                                                                                                                                                                                               /translation="MKIYGCISGLLEFVGLPCCWCTFYPCHAAEARNFTYISHGLGHV
HGHEGCRNFINVTHSAFLYLNPTTPTAPAITHCLLLVLAAKMEHPNATIWLQLQPFGY
HVAGDVIVNLEEDKRHPYFKLLRAPALPLGFVAIVYVLLRLVRWAQRCYL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLRYDEHTALYNCSASKTCHYCTFLDEOIIFFGTDCDDTYAYPVAEVLEQAHGPYSAL
FDDMPPFIYYGREFGIVVLDVFMFYPVLVLFFLSVLPYATLILEMCVSILFIIYGIYS
GAYLAMGIFAATLAIHSIVVLROLLWLCLAMRYRCTLHASFISAEGKVYPVDPGLPVA
                                                                                                                                     'translation="MGRAYSGPVALLCFFLYFCFICGSVGSNNTTICMHTTSDTSVHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MLSMIVLLFLLWGAPSHAYFSYYTAQRFTDFTLCMLTDRGVIAN
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Submitted (02-NOV-1993) M. Lipinski, Lab. de Biologie des Tumeurs
Humaines, CNRS URA 1156, Inst. Gustave Roussy, 94805 Villeuif
Cedex, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             788 catgatggtcacacttggatataccccagtgtgg-gtaaggttggggtattgcagggcct 846
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Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1319)
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H.sapiens mRNA for vacuolar H+ ATPase E subunit.
X76228
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11901. .12389
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/db_xref="PID:e265621"
/db_xref="PID:91835173"
/db_xref="GI:1835173"
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/db_xref="PID:e265622"
/db_xref="PID:g1835174"
/db_xref="GI:1835174"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _xref="PID:91835175"
_xref="GI:1835175"
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protein_id="CAA69183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2394 bp mRNA PRI 12-SEP-1998 dynamin-like protein Dymple isoform mRNA, complete
                                                                    Gaps
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Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar, Shano,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and Kikuchi,Y.
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         Length 1934;
                                                                                                     Length 834;
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                              Indels
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                              28;
         Score 66.2; DB 5;
Pred. No. 0.0016;
0; Mismatches 28;
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                                                                                                                                                          A/U388 834 bp DNA
Sequence 18 from Patent WO9811225.
A70388
                                                                                                                                                                                                                                                                                                                                                     /organism="unidentified"
/db_xref="taxon:32644"
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         y Match 7.1%;
Local Similarity 74.8%;
hes 83; Conservative
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Homo sapiens
                                                                                                                                                                                                                                       unidentified unclassified
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A70388.1
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          Query Match
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/db_xref="PID:93126874"
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/translation="MEALIPVINKLQDVFNTVGADIIQLPQIVVVGTQSSGKSSVLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIELQIRELILRFISNPNSIILAVTAANTDMATSEALKISREVDPDGGRTLAVITKLD
MADAGTDAMDVLAGRVIPVKLOIGVVNRSQLDINNKKSVTDSINDETREFALQKKYPSL
ANRNGTRVIARTLARHLEMHENCLPELKTR INVLAAQYQSLLNSYGEPVDDKSATLL
QLITKFATEYCNTIEGTAKYIETSELCGGARICYIFHERGRTLESVDDLGGLNTID
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TQELLRFPKLHDAIVEVYTCLLRKRLPVTNEMVHNLVAIELAYINTKHPDFADACGLM
NNNIEEQRRNRLARELPSAVSRDKVASGGGGVGDGVQEPTTGNWRGMLKTSKAEELLA
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DFDEIRQEIENETERISGNNKGVSPEPIHLKIFSPNVVNLTLVDLPGMTKVPVGDQPK
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                                                                                                                                                                                                                                                                                                                                                                                Submitted (18-APR-1998) Graduate Institute of Biochemistry, No.100, Shih-Chuan 1st Road, Raohsiung, Taiwan, ROC 80708, Taiwan, ROC Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="large G-protein; dyn IV; expressed in heart, brain, placenta, lung, liver, skeletal muscle, kidney and pancreas; 37 amino acid in frame deletion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPIMPASPQKGHAVNLLDVPVPVARKLSAREQRDCEVIERLIKSYFLIVRKN
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                                                                                                                      Hong Y.R., Chen,C.H., Cheng,D.S., Howng,S.L. and Chow,C.C.
Human dynamin-like protein interacts with the glycogen synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              835 attgcagggcctcccaacaatctcttaaataaataaagaagttgttcaggtaaaaaaa 894
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2394)
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                                                                                                                                                                                         Biochem. Biophys. Res. Commun. 249 (3), 697-703 (1998) 98401153
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Hong, Y.R., Chen, C.H., Cheng, D.S. and Chou, C.K.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .2394
Organism="Homo sapiens"
Ab_xref="taxon:9606"
/tissue_rype="liver"
/dev_stage="fetus"
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erential expression of four human dynamin-like protein variants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="large G-protein; alternatively spliced; expressed at low levels in brain, heart and kidney"
                                                                                                                                                                                 1 (Dases 1 to 2472)
Hong,Y.R. and Chen,C.H.
Direct Submission
Submitted (14-MAY-1999) Graduate Institute of Biochem Kaohsiung
Medical College, No. 100, Shih-Chuan 1st Road, Kaohslung 80708,
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2472)
                                                                     Chen, C.H., Hwang, S.L., Howng, S.L., Liao, C.H., Chou, C.K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product="dynamin-like protein DYNIV-11"
protein_id="AAD39541.1"
                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                               Location/Qualiflers
1. .2472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="DYNIV-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                jene="DYNIV-11"
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Gaps ; 0 Length 2472; Indels Ouery Match 7.0%; Score 65.6; DB 42; Best Local Similarity 76.9%; Pred. No. 0.0021; Matches 80; Conservative 0; Mismatches 24;

835 attgcagggcctcccaacaatctctttaaataaatgaaggtgttgttcaggtaaaaaaa 894 g

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Search completed: September 28, 1999, 16:39:42 Job time: 6969 sec

Sequence encoding Mus musculus Tub I

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on:

September 28, 1999, 16:45:17; Search time 303.81 Seconds (without alignments) 772.457 Million cell updates/sec

Title: Perfect score: Sequence:

IDENTITY_NUC Scoring table:

311585 segs, 125096042 residues Searched:

N_Geneseq_36:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			vel haemopoieti	oliced murine	Nucleotide sequenc	_	Novel haemopoietin	ത	Nucleotide segment	CDNA encoding rat	Nucleotide seguenc	cDNA encoding an a	Nucleotide seguenc	cDNA encoding huma	Expressed sequence	Equipe arteritis v	Equipe arteritis v	secreted	orphan re	Pot 1de sec	מינים מנילים	, ,	rostate-tumou	ate-timon	Gl prote	ld ofgH1	equence of mu	Immunode	from clon	n foetal b	t soluble	PKR gene	otide seq	adult br	Tinylendope	Asparaginylendopep	paraginylendope	ALP encodin	ta-specific	113 0 411	UMAN TUMOUT AN	n cathonein v	acid inv	one pice	ta-ene	וים בהביד ד
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Example 8: Page 99-100; 182pp; English.

NR6 is a novel haemopoletin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in
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Unspliced murine NR6 nucleotide sequence.
Haemopoletin receptor; cell proliferation; cell survival; therapeutic; neuronal proliferation; drug screenin Mouse.
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A, Nicola NA, F
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W09811255-A2.
19-MAR-1998.
11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS PTY LTD.
(DZIEV) DZIEKCLEWSKA H E.
Alexander W, Fabri L, Farley A, Hill
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Zhang J;
WPI; 98-260970/23.
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vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. products can also be used for detection and diagnosis, e.g. for or predisposition to cancers, or for drug screening. sequence 1930 Bp; 375 A; 623 C; 561 G; 371 T;
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                                                                     Length 1930
                                                                                         Indels
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Pred. No. 3.2e-160;
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100.0%; Pre
0;
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Matches 888)
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11463 GAGCCCCAGGTTTTACTGCATCATCAAGTTGCTGAAGGGTCCAGGCTTAATGTGGCCTCT
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WPI; 98-260970/23.
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The NR protein is a novel Haemopoletin receptor (HR). Interaction and the NR protein is a novel Haemopoletin receptor (Cells.) The HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.
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                                                                                                   cancer;
                                                       29-SEP-1998 (first entry)
Nucleotide sequence for murine NR6 containing additional 5N sequence.
Haemopoietin receptor; cell proliferation; cell differentiation; cancer cell survival; therapeutic; neuronal proliferation; drug screening; ss;
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                                                                                                                                                                                                                                                                                                                                    New isolated haemopoletin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells
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                                                                                                                                                                                                            11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS PTY LTD.
(DZIEC) DZIEGLEWAH H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Pred. No. 7.3e-132;
0; Mismatches 27;
V27148

DE V27148; 24.748 standard; DNA; 11832 BP AC V27148; DT 29-1998 (first entry)
DE Nucleotide sequence for murine KW Haemopoletin receptor; cell provided in the coll survival; therapeutic; new Mouse.

SM WS SP. 1994.

MOSB11225-A2.
PD 19-MAR-1998.
PF 11-SEP-1996; AU-002246.
PR 11-SEP-1996; AU-002246.
PR 11-SEP-1996; AU-002246.
PR AMRA-) AMRAD OPERATIONS PTY L PARANACH W. Fabri L. Farley A Darandew W. Fabri L. Farley A Darandew W. Fabri L. Farley A Darandew W. Fabri L. Farley A Darandew W. Fabri L. Farley A Darandew W. Fabri L. Farley A Darandew W. Fabri L. Farley A Darandew W. Fabri L. Farley A Darandew W. Fabri L. Farley A Darandew W. Fabri L. Farley A Darandew W. Fabri L. Farley A Darandew W. Fabri L. Farley A Darandew M. Nash A. Nic Danam J. September 19 20 Novel Hae CC Gerivatives can be used for mc CC derivatives can be used for mc CC corgulate development, maint CC derivatives can be used for modulation and survival. The products ce e.g. for cancers or predisposi Sequence 11832 BP; 2447 P.
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Best Local Similarity 96.3%;
Matches 778; Conservative
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The variation of survival of cells, respectively in the variation and survival of cells, respectively in the variation and survival of cells, responsible cells.

To mediating proliferation, differentiation and survival of cells, respectively cells.

Claim 8; Page 108-114; 182pp; English.

The NR6 gene encodes a novel Hemopoletin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, cells. The HR and it's products can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of cliferent cells and tissues in vitro and in vivo. They can be present in the appeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.

Sequence 6663 BP; 1462 A; 1852 C; 1715 G; 1634 T;
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11583 GACCTGGAGGCTCACCTGAATTGGAGCCCCTCTGTACC - ATCTGGGCAACAAAGAAACCT
                                                                                                                 gacctggaggctcacctgaattggagccctctgtacctatctgggcaacaaagaaact
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(AMEA-) AMEAD OPERATIONS PTY LTD.
(DZIEZ) DZIEGLEMSKA H E.
Alexander W. Fabri L., Farley A. Hilton DJ, Kikuchi Y.
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
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/*tag= a
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Nucleotide sequence of Murine NR6.
Haemopoietin receptor; cell proliferation; ce cancer; cell survival; therapeutic; neuronal
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V27140;
29-SEP-1998 (first entry)
Novel haemopoietin receptor NR6.1 gene.
Haemopoietin receptor; cell proliferation; cell difficell survival; therapeutic; neuronal proliferation;
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11-SEP-1997; G02479
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                                                                                                                   Now isolated haemopoletin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells is 182pp; English.

The haemopoletin receptor (HR) NR6.1 is a form of the novel HR NR6. Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in a array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for grup screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NR6.2 gene.
proliferation; cell differentiation; cancer;
neuronal proliferation; drug screening; ss;
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11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS PTY LTD.
(DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Koʻlima I, Maeda M, Nash A, Nicola NA, Rakar S, Willson
  L, Farley A, Hilton DJ, Kikuchi Y,
Nash A, Nicola NA, Rakar S, Willson
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/*tag= a
/product= "Haemopoietin receptor NR6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.5%; Score 305; DB 1; I
100.0%; Pred. No. 8.6e-50;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
Alexander W, Fabri
Kojima T, Maeda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 305; Conserv
                                                   , J;
98-260970/23.
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                                                                                                   P-PSDB; W55011.
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us-09-037-657-16.rng

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WO9849307-A1
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                                                        e.g. neuronal cells
Claim 5; Page 84-87; 182pp; English.
The haemopoletin receptor (HR) NR6.2 is a form of the novel HR NR6.
Interaction between the novel HR and a liqand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of the receptors e.g. different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.
Sequence 1673 BP; 344 A; 550 C; 474 G; 305 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1283 AGTTTCCGCCTGTACGACCAGTGGCGTGCTTGGATGCAGAAGTCACAAAAACCCGAAAC 1342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 agttccgcctgtacgaccagtggcgtgcttggatgcagaagtcacacaagacccgaaac 300
                                                                                                                                                                                                                                                                                                             Gaps
WPI; 98-260970/23.
P-PSDB; W55012.
New isolated haemopoletin receptor - used for developing products for modulating proliferation, differentiation and survival of cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine; U4 protein; haematopoietin receptor superfamily; cell proliferation; immune response; antibody; cell differentiation; autoimmune disease; cancer; allergy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding U4 haematopoietin receptor superfamily chain - potentially useful, e.g. for modulating cell proliferation or immune response, for treating cancer and auto:immune disease Claim 1; Pages 25-26; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              gcgggaatctggagcgagtggagccacccaccgctgcctccacccctcgaagtgagcgc
                                                                                                                                                                                                                                                                                                                                   1 ggcaccgtttacttcgtccaagtgcgttgtaacccattcgggatctatgggtcgaaaag
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16-JAN-1997; US-784863.
(GEMY ) GENETICS INST INC.
COLILIAS M, DONALGSON DD, Neben T, Whitters M;
                                                                                                                                                                                                                                                            32.4%; Scc...
100.0%; Pred. No...
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V41688;
26-cCT-1998 (first entry)
Nucleotide sequence of the murine U4 gene.
Murine; U4 protein; haematopoletin recepto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
122. .1399
/*tag= a
/product= "U4 protein"
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Best Local Similarity 100.
Matches 304; Conservative
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P-PSDB; W59804.
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This is the nucleotide sequence encoding the murine U4 protein from the haematopoletin receptor superfamily, used in the method of the invention for the modulation of cell proliferation, or the immune response. Transformed mammalian cells are used to produce recombinant U4 protein. The U4 protein is used to screen for specific binding agents, raise antibodies. It is also used as reagents for assays and as ilssue markers for isolation of cognate ligands and receptors, and in pharmaceutical compositions which may modulate cell proliferation, cell differentiation, and the immune system (e.g. for treating immune deficiency, inherited or the result of infection, autoimmune diseases, sequence 1656 BP; 318 A; 552 C; 478 G; 308 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1040 GGCACCGITTACITCGTCCAAGTGCGTTGTAACCCATTCGGGATCTATGGGTCGAAAAAG 1099
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CDNA encoding rat Zcytor5.

Zcytor5; cytokinin-like receptor; down-regulation; growth factor; maintenance factor; thyroid; heart; skeletal muscle; cardiotrophicardiac pathology; heart enlargement; Zcytor5 ligand; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                     32.4%; Score 304; DB 1; Length 1656; 100.0%; Pred. No. 1.3e-49; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Disclosure; Page 72-75; 55pp; English.
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159. .1436
/*tag= a
/product= Zcytor5
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Adams RL, Foster DC, Gilbert T,
Lok S, Presnell SR, Whitmore TE;
WPI: 99-03462/03.
P-PSDB; W70862.
                                                                                                                                                                                                                                                                                                                318 A;
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Best Local Similarity 100.0
Matches 304; Conservative
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13-FEB-1998; US-023890.
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01-MAY-1997; US-045287
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New isolated haemopoietin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells claim 7; Page 102-104; 182pp; English.
The NR6 gene encodes a novel Haemopoietin receptor (HR). Interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ccgggcccgggcggcgggtgtgcgagccgcggggcggcgagcccagctcgggcccggtg 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agtttccgcctgtacgaccagtggcgtgcttggatgcagaagtcacacaagacccgaaac 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gogggaatctggagcgagtggagccacccaccgctgcctccaccctcgaagtgagcgc 120
The present sequence encodes a protein designated Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and therapeutically to modify Zcytor5 ligand effects. Sequence 1724 BP; 350 A; 550 C; 500 G; 324 T;
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Nucleotide sequence of clone HFK-66 encoding human NR6.
Haemopoietin receptor; cell proliferation; cell differentiation; can cell survival; therapeutic; neuronal proliferation; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCGGGAATCTGGAGCGAGTGGAGCCACCCCACCGCTGCTCCACCCCTCGAAGTGAGCGC
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                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                           Score 297.6; DB 1;
Pred. No. 2.2e-48;
0; Mismatches 4;
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1. 1053
/*tag* a
/product* "Human NR6"
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98.78;
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V27144;
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11-SEP-1996; AU-002246.
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between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to requiate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening. Sequence 1391 BP; 281 A; 459 C; 417 G; 234 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA encoding an allelic varaint of human Zcytor5.
Zcytor5, cytokinin-like.receptor; down regulation; growth factor;
maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-l;
cardiac pathology; heart enlargement; Zcytor5 ligand; allelic varaint;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 cggcgcgagctcaagcagttcctcggctggctcaagaagcacgcatactgctcgaacctt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        682 GGCACCGTGTACTTCGTGCAAGTGCGCTGCAACCCCTTTGGCATCTATGGCTCCAAGAAA
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                                                                                                                                                                                                                                                                                                                          Length 1391;
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01-MAY-1999; U08865.

13-FEB-1998; US-074721.

01-MAY-1997; US-850030.

13-FEB-1998; US-223890.

(ZYMO) ZYMOGENETICS INC.

Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,

Lok S, Presnell SR, Whitmore TE;

WPI: 99-034662.
                                                                                                                                                                                                                                                                                                                          ; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                    42;
                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                       Score 249.8;
Pred. No. 2.4
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/product= Zcytor5
                                                                                                                                                                                                                                                                                                                       26.6%;
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                                                                                                                                                                                                                                                                                                                          Query Match 26.6
Best Local Similarity 86.8
Matches 275; Conservative
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Zcytor5, which
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administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe and integrity of the Zcytor5 gene on chronsome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcytor5 and therapeutically to modify Zcytor5 ligand effects. Sequence 1813 BP; 415 A; 604 C; 519 G; 275 T;
                                                                                                                                                                                                                                                                                                                      994 GCCACCGTGTACTICGTGCAAGTGCGCTGCAACCCCTTTGGCATCTATGGCTCCAAGAAA 1053
                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding U4 haematopoietin receptor superfamily chain - potentially useful, e.g. for modulating cell proliferation or immune response, for treating cancer and auto:immune disease (laim 1, page 28; 38pp; English.

This is the nucleotide sequence encoding the human U4 protein from the haematopoietin receptor superfamily, used in the method of the invention for the modulation of cell proliferation, or the immune response. Transformed mammalian cells are used to produce recombinant U4 protein. The U4 protein is used to screen for specific binding agents, raise antibodies. It is also used as reagents for assays and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1234 AGCTICCGCCTCTACGACCAGIGGCGAGCCTGGAIGCAGAAGTCGCACAAGACCCGCAAC 1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
                                                                                                                                                                                                                                                                                                                                                                                                                                 ccgggcccgggcggcggtgtgcgagccgcggggcgggcgagcccagctcgggcccggtg 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 agtttccgcctgtacgaccagtggcgtgcttggatgcagaagtcacacaagacccgaaac 300
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                       ggcaccgtttacttcgtccaagtgcgttgtaacccattcgggatctatgggtcgaaaaag 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, U4 protein, haematopoletin receptor superfamily,
cell proliferation; immune response; antibody; cell differentiation;
autoimmune disease; cancer; allergy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cggcgcgagctcaagcagttcctcggctggctcaagaagcacgcatactgctcgaacctt
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                                                                                                                                                                                                                       Length 1813;
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                                                                                                                                                                                                               Score 249.8; DB 1;
Pred. No. 2.5e-39;
0; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JAN-1998; U00334.
16-JAN-1997; US-784863.
(GEMY ) GENETICS INST INC.
WPI; 98-414109/35.
P-PSDB; W59805.

    1228
    *tag= a
    /product= "U4 protein"

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Nucleotide sequence of the human U4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                 26.6%;
86.8%;
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Best Local Similarity 86.8
Matches 275; Conservative
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V41689
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989 CCGGGCCCGGGCGGGGGGGGGGAACCGGGGGGGGGGAGAGCCGAGCTCGGGGCCGGTG 1048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as tissue markers for isolation of cognate ligands and receptors, and in pharmaceutical compositions which may modulate cell proliferation, cell differentiation, and the immune system (e.g. for treating immune deficiency, inherited or the result of infection, autoimmune diseases, sequence 1579 BP; 304 A; 535 C; 473 G; 267 T;
                                                                                                                                                                                                                                                                                                                                           cggcgcgagctcaagcagttcctcggctggctcaagaagcacgcatactgctcgaacctt 240
                                                                                                                                                                                                                                    869 GCCACCGTGTACTTCGTGCAAGTGCGCTGCAACCCCTTTGGCATCTATGGCTCCAAGAAA 928
                                                                                                                                                                                                                                                                       gcgggaatctggagcgagtggagccacccaccgctgctccacccctcgaagtgagcgc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V70894;
17-MAR-1999 (first entry)
CDNA encoding human Zcytor5.
Zcytor5; cytokinin-like receptor; down-regulation; growth factor; maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-l; Homo saplens.
                                                                                                                                                                          Gaps
                                                                                                                                                                                                   1 ggcaccgtttacttcgtccaagtgcgttgtaacccattcgggatctatgggtcgaaaag 60
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New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g
down-regulating Zcytor5 natural ligands or detecting cardiotrophin-1
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The present sequence encodes a protein designated Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the
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                                                                                                                                           Length 1579;
                                                                                                                                                                          Indels
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01-MAY-1997; US-045287.
01-MAY-1997; US-850030.
13-FEB-1998; US-023890.
(ZYMO ) ZYMCGENETICS INC.
Adams RL, FOSTER DC, Glibert T, Jelmberg AC, Lehner Con S, Presnell SR, Whitmore TE;
P-PSDB; W70860.
                                                                                                                                 Ouery Match 26.6%; Score 249.6; DB 1;
Best Local Similarity 88.8%; Pred. No. 2.7e-39;
Matches 270; Conservative 0; Mismatches 34;
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/*tag= a
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32; Indels

Score 92.8; DB 1; Pred. No. 1.1e-09; 0; Mismatches 32;

9.9%;

Length 259

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therapeutically to modify 2cytor5 ligand effects. Sequence 259 BP; 53 A; 64 C; 81 G;
                                                                                                  Query Match
Best Local Similarity 76.8
Matches 106; Conservative
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Best Local S:
Matches 108
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V09039
ID V09039
AC V09039
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blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcytor5 and the therapeutically to modify Zcytor5 ligand effects. Sequence 1690 BP; 319 A; 592 C; 505 G; 274 T;
                                                                                                                                                                                                                                                                                                                                                                                                           961 GCCACCGTGTACTTCGTGCAAGTGCGCTGCAACCCCTTTGGCATCTATGGCTCCAAGAAA 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGGCGCGAGCTCAAGCAGTTCCTGGGCTGGCTCAAGAAGCACGCGTACTGCTCCAACCTC 1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ccgggcccgggcggcgggtgtgcgagccgcgggggcggcgagcccagctcgggcccggtg 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g. down-regulating Zcytor5 natural ligands or detecting cardiotrophin-1
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                              ggcaccgtttacttcgtccaagtgcgttgtaacccattcgggatctatgggtcgaaaaag
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Expressed sequence tag used to identify human Zcytor5.
Expressed sequence tag used to identify human Zcytor5.
Exprors; cytokinin-like receptor; down-regulation; growth factor; maintenance factor; thyroid; heart; skeletal muscle; cardiotrophicardiac pathology; heart enlargement; Zcytor5 ligand; EST; ss.
                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                        Length 1690;
                                                                                                                                                                                                                                                           34; Indels
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                                                                                                                                                                                                   26.6%; Score 249.6; DB 1
llarity 88.8%; Pred. No. 2.7e-39;
Conservative 0; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 77; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V70897 standard; cDNA; 259 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-FEB-1998; US-074721.
01-MAY-1997; US-045287.
01-MAY-1997; US-850030.
13-FEB-1998; US-023890.
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01-MAY-1998; U08865.
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Best Local Similarity
Matches 270; Conserv
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                                                                           119 GGCANCGTGTACTTCGTGCAAGTGCGCTGCAANCCCTTTGGCATCTATGGCTNCAAGAAA 178
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12-JUL-1997: NLO408.
12-JUL-1996: NL-003579.
(UVLE-) RIJKSUNLY LETDEN.
Bredenbeek RJV. Wassenaar ALM:
Van Dinten LC, Wassenaar ALM:
Van Jin596/LO.
Recombinant DNA vector that produces infectious RNA of equine arterits virus - and derived RNA, host cells and virus particles,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       catgatggtcacacttggatataccccagtgtgg-gtaaggttggggtattgcagggcct
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                                                                                                                                                                                                                                                                                           sequence.
therapy; ss.
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Pred. No. 2.2e-05;
0; Mismatches 43;
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detection;
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                                                                                                                                                                                                                                                                       21-JUL-1998 (first entry)
Equine arteritis virus partial
equine arteritis; genome; EAV;
Equine arteritis virus.
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                                                                                                                                                                                                                                          V09036 standard; RNA; 12827 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.6%; al Similarity 71.1%; 108; Conservation
                                                                                                                            121 ccgggcccgggcgggg 138
                                                                                                                                                         239 CNGGGCCCGGGNGGNGGG 256
                                                                                                                                                                                                                                                                                                                                         WO9802549-A1.
22-JAN-1998.
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21-JUL-1998 (first entry)
Equine arteritis virus expression vector pEAV030.
equine arteritis; genome; EAV; detection; therapy; cyclic; circular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ecombinant DNA vector that produces infectious RNA of equine interitis virus - and derived RNA, host cells and virus particles,
                                                                                                                                                                                                                                                                                                                                "synthetic sequence with unique XhoI site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence is that of of a recombinant DNA vector, pEAV030, comprising a DNA sequence complementary to part of the genome of equine arteritis virus (EAN) which has adjacent to its 3'-end a non-EAV specific promoter for a non-EAV specific RNA polymerase. It can be used to make viral particles and for therapeutic use. The vector can be stably incorporated into host cells and produces infectious RNA.

3912 G; 3972 G; 4123 T;
                                                                                                                                                                                                                                                      "Bacteriophage T7 promoter sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UYLE-) RIJKSUNIV LEIDEN.
redenbeek PJ, Den Boon JA, Snijder EJ, Spaan WJM,
an Dinten LC, Wassenaar ALM;
                                                                                                                                                                                                                                                                                                                                                                                                          "pUC18 vector sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapeutically
1; Pages 21-24; 36pp; English.
                                                                                                                                                                                Location/Qualifiers
15512. .15528
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                                                                                                      Equine arteritis virus.
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12845.
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1; Gaps Score 71.2; DB 1; Length 15528; Pred. No. 2.2e-05; 0; Mismatches 43; Indels 1; 43; Indels 7.6%; 71.1%; Ouery Match Best Local Similarity 71.1 Matches 108; Conservative

12635 CAGGGCCGTAAGACGTGGATATTCTCCTGTGTGGCGTCATGTTGAAGTAGTTATTAGCCA 12694 788 catgatggtcacacttggatataccccagtgtgg-gtaaggttgggggtattgcagggcct 846 a a

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12755 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 12786 907 ааааааааааааааааааааааааааааа 938 g ò

Search completed: September 28, 1999, 16:45:44 Job time: 7329 sec

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September 28, 1999, 16:39:36; Search time 152.56 Seconds (without alignments) 563.664 Million cell updates/sec
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/cgn2_6/ptodata/2/ina/5D_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS9_COMB.seq:*
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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd
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US-08-143-219-1
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US-08-467-607-2
US-08-850-392-2
PCT-US4-1090-5
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1-441-9 -08518- -12883- 1-405-1 1-850-1 5-716-1 2-411A-	NTS	· ມ ບ ര	tch 6.8%; Score 64; DB 4; Length 10660; 100; Conservative 0; Mismatches 60; Indels 0; G ttggtccacatgatgatacacactgatgatacaccagtgtgggtaagtttggggtattg
US-08-461-441 PCT-US93-0851 PCT-US94-1288 US-08-344-405 US-08-384-850 US-08-865-716 US-08-471-717	ALIGNMENT	267803B .W. Sequence for Spir and Method for sch, Gebhardt & Sch, Gebhardt &	re 64; DB d. No. 8.7 Mismatches atatacccca 1 Ca TTTAATAAA aaataaagga
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11172 11172 11813 3200 3200 1147 1898		T. 1 -267-803B-8 uence 8, Application US/08267803 uence 8, Application US/08267803 NERL INFORMATION: APPLICANT: Chung, Ming-yl APPLICANT: Ranum, Laura P.W. APPLICANT: Ranum, Laura P.W. APPLICANT: Coghbi, Huda Y. APPLICANT: Chung, Ming-yl TITLE OF INVENTION: Gene Sequence of Invention of Sequence of Se	larity 62.7 Conservative. Conservative. Cacatgatggtcc I CanaarTTGaaC tcccaacaatctc
eeemme e		NN: Harry Ha	Y rva gat gat hrrr Ara
99999999		LT 1 8-267-803B-8 guence 8, Application US guence 8, Application US guence 8, Application US guence 8, Application US APPLICANT: Carr, Harry APPLICANT: Carr, Harry APPLICANT: Caphbi, Hud APPLICANT: Caphbi, Hud APPLICANT: Caphbi, Hud APPLICANT: Caphbi, Hud TITLE OF INVENTION: Ge tent No. 584183 TITLE OF INVENTION: Ty NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS: 8 CORRESPONDENCE DADRESS: 8 COMPUTAY: USA COMPUTAY: USA COMPUTAY: IBM PC COMPUTAY: USA COMPUTAY: END COMPUTAY: END COMPUTAY: USA COMPUTAY: LA APPLICATION NUMBER: 28-UN- CLASSIFICATION: 435 ATTORNEY/AGENT INFORMAT NAME: MCCOTMACY/AGENT INFORMAT NAME: MCCOTMACY/AGENT INFORMAT RELEPANCE: G12-305-122 NUMBER: CAPACTERISTIC LENGTH: 10660 base p TYPE: NUCLASS: SIGILE TOPOLOGY: 111cat NAME/KEY: CDS LOCATION: 936.3384 8-267-803B-8	Similarity O; Conser ggtccacatg Garrcaaar ggcctcccaa refrireagn
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5173 base pairs
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
                                                                                                                                                                                                                                                              CILL.
STATE: IA
COUNTRY: USA
77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION:
US-08-242-677-1
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Pred. No. 8.5e-06;
                                                                                                                        APPLICANT: Takashita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Anani, Bon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                       ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
ZIP: 10005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02481.1323-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN: osteoblastic cell line MC3T3E1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-0CT-1996
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 0248:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: CDNA to MRNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3581 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.8%;
ilarity 82.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: 284..2671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity <sup>f</sup>
Treates 73; Conservat
                                                                                                                                                                                                                                                                                                                                                        COUNTRY: D.C.
ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . LOCATION:
US-08-738-349-1
                                                       RESULT 2
US-08-738-349-1
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GENERAL INFORMATION:
APPLICANT: Gaynor, Richard B
APPLICANT: Wu, Foon W.
TITLE OF INVENTION: Cellular Nucleic Acid Binding Protein
TITLE OF INVENTION: and Uses Thereof in regulating Gene Expression and in the
TITLE OF INVENTION: Treatment of AIDS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 63.2; DB 2;
Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                           SEE: Arnold, White & Durkee : P.O. Box 4433 Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5133 AAAAAAAAAAAAAAAAAAAA 5156
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Katze, Michael G.
Roy, Sophie
Koromilas, Antonis E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08143219
Patent No. 5670330
GENERAL INFORMATION:
APPLICANT: Sonenberg, Nahum
APPLICANT: Ratze, Michael G.
APPLICANT: Roy, Sophie
APPLICANT: Roy, Sophie
RESULT 3
US-08-242-677-1
Sequence 1, Application US/08242677
; Patent No. 5677143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732
REFRENCE/DOCKET NUMBER: UTSD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 84.5%;
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 713-789-2679
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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us-09-037-657-16.rni

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6.6%; Score 61.6; DB 4; Length 270;
88.2%; Pred. No. 9.7e-06;
tive 0; Mismatches 9; Indels
                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/520,678A
                              E: Howell & Haferkamp, L.C. 7733 Forsyth Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ANDERSON, JOHN
APPLICANT: CHRYSLER, SUSANNA
TITLE OF INVENTION: NOVEL CATHEPSIN
TITLE OF INVENTION: COMPOSITIONS FOF
WOMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Henderson, Melodie W.
REGISTRATION NUMBER: 37,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 6C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            800 F. Gateway Blvd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: DNA (genomic)
US-08-520-678A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 800 F. commission CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH: 270 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 AAAAAAAAAAAAA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 314-727-6092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JAY S.
            CORRESPONDENCE ADDRESS:
                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
                                        STREET: 7/35
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Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                     COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Pred. No. 1.2e-05;
0; Mismatches 9; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rice, Charles M.
PPLICANT: Kolykhalov, Alexander A.
TITLE OF INVENTION: NOVEL 3' TERMINAL SEQUENCE OF HEPATITI.
TITLE OF INVENTION: C VIRUS GENOME AND DIAGNOSTIC AND THER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
PLICANT: Barber, Glen N.
TLE OF INVENTION: TUMOR-CELL ASSAY METHOD AND KIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: HUMAN PKR GENE, FIGURE 5
                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/141,24
FILING DATE: October 22, 1993
FILING DATE: September 29, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                         PC-DOS (Version 5.0)
                                                                                                                                                                                                                                                                          WordPerfect (Version 5.1)
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/143,219
FILING DATE: October 25, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 22,798
REFERENCE/DOCKET NUMBER: 204/139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08520678A
                                                                             ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.7%;
Best Local Similarity 88.3%;
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2592 AAAAAAAAAAAAA 2608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2628 base pairs
nucleic acid
EDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Douglas E. Olson
                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                          COMPUTER READABLE FORM MEDIUM TYPE: 3.5" D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                   Los Angeles
CA
                                                                                                                                                                                                                                 COMPUTER: IBM COMPOPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         FICATION:
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                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
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1373 TCMCCATTCTTATTTCACYTTAGRATCMAGGGTGGGRGRGRGRGGGGGGGGAGTTGTCART 1432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MCCONLOGUE, LISA
APPLICANT: SEMKO, CHRISTOPHER M.F.
TITLE OF INVENTION: NOVEL CATHEPSIN AND METHODS AND
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,392 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1493 AAAAAAAAAAAAAAAGAAAAAAAAAAAAAAAAA 1527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,362
FILING DATE: 06-JUN-1995
ATTORNEY-AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEE: ATHENA NEUROSCIENCES: 800 F. Gateway Blvd. South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08850392
Patent No. 5858982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: TUNG, JAY S. APPLICANT: SINHA, SUKANTO
                                                         1558 base pairs
                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: DUVALL, JEAN M. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
                                                                               nucleic acid
                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94080
                                                                                                                                                                         ; NAME/KEY:
; LOCATION:
US-08-469-362-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-850-392-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: TUNG, JAY S.
APPLICANT: SINHA, SUKANTO
APPLICANT: SINHA, LISA
APPLICANT: SEMKO, CHRISTOPHER M.F.
TITLE OF INVENTION: NOVEL CAPHEPSIN AND METHODS AND
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8e-05;
nes 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
6.5%; Score 61.4; DB 3;
Best Local Similarity 55.5%; Pred. No. 1.8e-05;
Matches 86; Conservative 13; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1493 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Mismatches
                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DUVALL, JEAN M.
REGISTRATION NUMBER: 32,731
REFERENCE/DOCKET NUMBER: 002010-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 877-0900
TELEPHONE: (415) 877-0900
TELEPHONE: (415) 877-0370
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/469,362 FILING DATE: 06-JUN-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: ATHENA NEUROSCIENCES
STREET: 800 F. Gateway Blvd.
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08469362
Patent No. 5849711
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: DUVALL, JEAN M. REGISTRATION NUMBER: 32,731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
06-JUN-1995
N: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                  STRANDEDNESS
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LOCATION:
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Length 3238;

6.58;

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                                                                                                                                                                                                                                                                                                     1373 TCMCCATTCTTATTTCACYTTAGRATCMAGGGTGGGRGGRGGGRGGGAGGGAATTGTCART 1432
                                                                                                                                                                                                           784 tccacatgatggtcacacttggatataccccagtgtgggtaaggttgggggtattgcaggg 843
                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                           Length 1558;
                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute Inc.- Legal Affairs
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
URRENT APPLICATION DATA:
                                                                                                                                                      1.8e-05;
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                                                                                                                                                                            13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: GENETICS INSTITUTE, INC.
TITLE OF INVENTION: RECEPTOR PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US94/10080
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATION NUMBER: US 08/123,934
DATE: 17-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R
REGISTRATION NUMBER: 32,618
REFERRNCE/DOCKET NUMBER: 520;
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32,618
                                                                                                                                       55.58;
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MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: CFK1-10a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 3238 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (617) 498-82
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO:
                                                                                                                                                        Best Local Similarity 55.59
Matches 86; Conservative
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION DATA:
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EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                     CDS
103..1011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cambridge
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LOCATION:
PCT-US94-10080-5
                                                   ; NAME/KEY:
; LOCATION:
US-08-850-392-2
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                                  Score 61; DB 5; Length 323
Pred. No. 2.8e-05;
0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Nishikura, Kazuko
IIILE OF INVENTION: RNA Editing Enzyme and Methods of
IIILE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spring House Corporate Cntr, P.O. Box 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/280,443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 60.8; DB:
Pred. No. 3.9e-
0; Mismatches
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APPLICATION NUMBER: US 08/197,794
FILLING DATE: 17-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                               3187 AAAAAAAAAAAAAAAAAAAATA 3211
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Patent No. 5643778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Howson and Howson
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.5%;
Best Local Similarity 80.7%;
Matches 71; Conservative
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Query Match
Best Local Similarity 82.4.
The conservative 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 215-540-581
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155..3832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Spring House
STATE: Pennsylvania
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APPLICANT: NIShik
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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; LOCATION:
US-08-280-443-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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Length 6671;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE: Spring House Corporate Cntr, P.O. Box 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                 NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P.O. Box 457
CITY: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEE: Howson and Howson
: Spring House Corporate Cntr, P.O. Box 457
Spring House
                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; DB 3;
3.9e-05;
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                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,794
FILING DATE: 17-FEB-194
PRIOR APPLICATION NUMBER: US 08/280,443
FILING DATE: 25-UL-194
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,459
FILING DATE: 01-UNH-195
ATTORNEY/AGENT INFORMATION:
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of Use Thereof
                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 31,21:
REFERENCE/COCKET NUMBER: W:
TELECOMUNICATION INFORMATION
TELEPHONE: 215-540-9206
TELEFAX: 215-540-9206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 80.73
Matches 71; Conservative
                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bak, Mary E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
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MOLECULE TYPE:
                                                                                                                                                                                                                  MEDIUM TYPE:
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                                                                                                                                                                       19477
                                                                                                                                                   COUNTRY:
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Pred. No. 3.9e-05;
0; Mismatches 17; Indels 0
                                                                                                                                               NPPLICANT: Nishikura, Kazuko
IITLE OF INVENTION: RNA Editing Enzyme and Methods of Use
IITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                          SSEE: Howson and Howson
T: Spring House Corporate Cntr, P.O. Box 457
Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Nishikura, Kazuko
TITLE OF INVENTION: RNA Editing Enzyme and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNDBER: US 08/197,794
FILING DATE: 17-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/280,443
FILING DATE: 25-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6598 AAAAAAAAAAAAAAAAAAAAAAA 6625
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                                                                                  pplication US/08457459
                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
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REFERENCE/DOCKET NUMBER: WS'
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Best Local Similarity 80.7
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                             NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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155..3832
                                                                                                                                                                                                                                                                                                                      Pennsylvania
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY:
; LOCATION:
US-08-457-459-1
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Gaps

RESULT 12 US-08-555-678-1 Patent No.

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GENETIC SEQUENCES AND PROTEINS RELATED TO ALZHEIMER'S DISEASE 183
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                          6; DB 1;
2.9e-05;
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Pred. No. 2.9e-
0; Mismatches
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APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 136, Application US/08967101
Patent No. 5840540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
                                                                                                                                                                                                                                                               TOPOLOGY: both
MOLECULE TYPE: DNA (genomic)
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                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.5
Best Local Similarity 79.1
Matches 72; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HU
STREET: H1gh Street
                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U.S.A.
                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: 9...
US-08-473-981A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARFLICANT: Spilnger, Timothy A
TITLE OF INVENTION: METHODS OF IDENTIFYING AGENTS WHICH MODULATE
TITLE OF INVENTION: ICAM-3 BINDING TO LFA-1 (AS AMENDED)
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US95/02275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNDER: US 08/280,443
APPLICATION UNDER: US 08/280,443
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/197,794
FILING DATE: 17-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/CDCKET NUMBER: WST49BPCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
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Patent No. 5629162
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Best Local Similarity 80...
Thes 71; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 6671 base pair
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STRANDEDNESS: double
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MEDIUM TYPE: Floppy
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                         OPERATING SYSTEM:
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; LOCATION:
PCT-US95-02275-1
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Length 1817;

Indels

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LENGTH: 2285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                     o.to

, MOLECULE TYPE: CDNA

US-08-967-101-136
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ô 0; Gaps Score 60.6; DB 4; Length 2285; Pred. No. 3.1e-05; 0; Mismatches 12; Indels 0; Query Match
Best Local Similarity 84.6%;
Matches 66; Conservative (

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Search completed: September 28, 1999, 16:40:05 Job time: 6991 sec

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AA039053/c
LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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                                                                                                                                                                                                            Contact: Marra M/Mouse EST Project
Washugton University School of MedicineP
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Final: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.linl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 gcgagtggagccacccaccgctgcctccaccctcgaagtgagcgcccgggcccgggcg 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 gcggggtgtgcgagccgcggggcggcgagcccagctcgggcccggtgcggcgagctca 193
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                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 503)
                                                                                                                                                                      Unpublished (1996)
On Dec 30, 1996 this sequence version replaced g1:1528949.
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Pred. No. 2e-35;
0; Mismatches 4; Indels 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                            Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 486.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="IMAGE:479046"
/clone_llb="Soares mouse
                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
                                                                                                                                             Waterston, R.
The WashU-HHMI Mouse EST Project
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Matches 283; Conservative
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                              ORGANISM
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ORIGIN
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JOURNAL
COMMENT
KEYWORDS
SOURCE
                                                                      REFERENCE
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//OCE="Vector: pi773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5] represented with a Not I - oligo(dT) primer [5] represented with a Not I - oligo(dT) primer [5] represented with a Not I - oligo(dT) primer [7] represented and a Not I - on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos (total RNA provided by Minoru Ko, Wayne State Univ., from 2 ); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 445)
Marra, Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kücaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@lmage.llnl.gov) for further information.
                                                                                                                                                                                                                AA039053 445 bp mRNA EST 29-AUG-1996 mi99d07.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone_IMAGE:474733 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH108"
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Pred. No. 1.6e-34;
0; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
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Location/Qualifiers
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/clone="IMAGE:474733"
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M.Fatima Bonaldo.
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ilarity 96.6%;
Conservative
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Fax: 314 286 1810
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RESULT 1
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NID
VERSION
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                                                                                                                                                                                                                                                                                                                              GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd
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9D_est1:*

9D_est2:*

9D_est5:*

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em_est12:
em_est13:
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em_est17:
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gb_est29:
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em_est21:
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gb_est27
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gb_est31
gb_est32
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Perfect score:
Sequence:
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                                                                                                                                OM nucleic
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54: em_est23:*
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58: em_est23:*
58: em_est23:*
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59: em_est23:*
59: em_est23:*
50: em
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AAU49278 503 bp mRNA EST 30-DEC-1996 m145c04.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:479046 5', mRNA sequence.

GI:1755309

g1755309 AA049278.1

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Eutheria; Nedentia; Sciurognathi; Muridae; Murinae; Mus.
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 262)
S Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Ito, M., Aizawa, K., Akahira, S., Akiyama, J., Fekuda, S., Fukunishi, Y.; Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Itoh, M., Izawa, M., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigamco, Y., Shirata, Y., Shibata, Y., Shigamco, Y., Shirata, Y., Yamamura, T., Yokota,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genome-resertc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Scl. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Scl. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                        265 AGGICCIGCCGGCIAAACICIAAGGAIAGGCCAICCICCIGCIGGGICAGACCIGGAGGC 206
                                                                                                                                                                                                                                            750 ggggcacaatgagctcccacaaccacagctttggtccacatgatggtcacacttggatat 809
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/clone="1500034F20"
/clone_lib="Mus musculus adult C57BL/6J cerebellum"
                                                                                                                                                            205 TCACCTGAATTGGAGCCCCTCTGTACC-ATCTGGGCAACAAGAAACCTACCA-GAGGCT
                                                                                                                                                                                                                                                                                      Koyadai, Tsukuba, Ibaraki 305-0074, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="cerebellum"
/dev_stage="adult"

    .262
    /organism="Mus musculus"

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Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Chie Owa
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ORIGIN
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AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates: Catarrhini; Hominidae; Homo.

1 (bases 1 to 458)

Hillieri, Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Mardis, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schallenbarg, K., Soares, M.B., Tan, F., Thierry-Meg, J. Travaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1219 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAO43001 458 bp mRNA EST 10-MAY-1997 zk56£01.rl Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486841 5', mRNA sequence.
                                                                                                                                                                                                                               119
                                                                                         629 caggiccigccggctaaactctaaggataggccatcctcct-gcigggicagacciggag 687
                                                                                                                                                                                   747
                                                                                                                                                                                                                                                               748 ctggggcacaatgagctccacacaccacagctttggtccacatgatggtcacacttggat 807
                                                                                                                                                                                                                                                                                                                                                                867
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                                                                                                                                       61
                                                                                                                geteacetgaattggageeeetetgtacetatetgggeaacaaagaaacetaceatgagg
                                                                                                                                                                                                                                                                                                           120 CTGGGGCACAATGAGCTCCCACAACCACAGCTTTGGTCCACATGATGGTCACACTTGGAT
                                                                                                                                                                                                                                                                                                                                                       808 ataccccagtgtgggtaaggttggggtattgcagggcctcccaacaatctctttaaataa
                                                                                                                                                                                                             62 GCTCACCTGAATTGGAGCCCCTTGTACC-ATTTTGGCAACAAAGAAACCTACCA-GAGG
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    Length 262;
                                                  Indels
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                                                18;
    DB 50;
    Score 194.2; DB 5
Pred. No. 1.7e-27;
0; Mismatches 18
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High quality Sequence stop: 305.
Location/Qualifiers
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Query Match 20.7%;
Best Local Similarity 91.9%;
Matches 238; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 868 ataaaggagttgttcaggt 886
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AA043001/c
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Query Match
Best Local Similarity
Matches 223; Conserv
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      source
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KEYWORDS
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AA925924/c
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TITLE
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                 Not
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the No and Eco RI sites of the modified p1773 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo." 8 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:216609
                                                                                                                                                                                                                                                              184 egegageteaageagtteeteggetggeteagaageaegeataetgetegaacett-ag 242
                                                                                                                                                                                                                                                                                                                                   ggaatctggagcgagtggagccacccaccgctgctccaccctcgaagtgagcgcccg 123
                                                                                                                                                                                                                                                                                                                                                                                                   ggcccgggcggggtgtgcgagccgcgggggggggggcgagcccagctcgggcccggtgcgg 183
                                                                                                                                                                                                                                    Gaps
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Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 CGCGAGCTCAAGCAGTTCCTGGGCTGGCTCAAGAAGCACGCGTACTGCTCCAACCNTCNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W17583 390 bp mRNA EST 10-SEP-;
mb75b01.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 tttccgcctgtacgaccagtggcgtgcttggatgcagaagtcacacaagacccg 296
                                                                                                                                                                                                                                   4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1996)
On May 9, 1995 this sequence version replaced g1:804170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Excest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                             Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 others
                                                                                                                                                                                           20.0%; Score 187.6; DB 27; Length
85.7%; Pred. No. 3.1e-26;
ive 0; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 384.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMAGE:335209 5', mRNA sequence.
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W17583.1 GI:1291995
                                                                                                                                                                                                                               Matches 252; Conservative
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                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                 Best Local
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JOURNAL
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Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 315 8250
Fax: 319 315 956
Email: msoares@blue.weeg.uiowa.edu
The sequence tag present in the cDNA between the NotI site and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 TCACCTGAATTGGAGCCCCTCTGTACC-ATCTGGGCAACAAAAAAAACTACCA-GAGGCT 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA925924- 455 bp mRNA EST 07-FEB-1999
UI-R-Al-es-g-11-0-UI.S1 UI-R-Al Rattus norvegicus CDNA clone
UI-R-Al-es-g-11-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tcacctgaattggagcccctctgtacctatctgggcaacaaagaaacctaccatgaggct
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T
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                                                                                                                                                                                                                                                                                                                                                                                            Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches
                                                                                                                                                                                                                                                                                                                                                                                            56;
                                                                                                                                                                                                                                                                                                                                                                                          19.8%; Score 185.4; DB 26;
llarity 95.7%; Pred. No. 7.8e-26;
Conservative 0; Mismatches 6;
/organism="Mus musculus"
/db_xref="taxon:10090"
/map="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Res. 6 (9), 791-806 (1996)
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Rat

MD 20850, USA

FEATURES

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EST 30-OCT-1998
Bento Soares Rattus sp. cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Normalized rat kidney, Bento Soares"
/note="Organ: Kidney; Vector: pT/T3Pac; Site_l: EcoRI;
Site_2: NotI"
143 c 124 g 115 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 agccgcggggggggggggccagctcgggcccggtgcggcgcgagctcaagcagttcctcg 205
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Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & 1
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    On May 8, 1995 this sequence version replaced gi:801255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 151; DB 43; Length 470;
Pred. No. 2.3e-19;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arcc...
The Institute for Genomic Research
9712, Medical Center Drive, Rockville,
Tel: (301) 838-3529
Fax: (301) 838-0208
Email: nhlee@tigr.org
                                                                             1 470 bp mRNA
99 Normalized rat kidney,
3' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Rattus sp."
/db_xref="taxon:10118"
/clone="RKIDD49"
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AI233311.1 GI:3817191
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96.9%;
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1 (bases 1 to 229)
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Rattus sp.
Rattus sp.
                                                                                                 EST229999 1
RKIDD49 3'
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Matches 154
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                                                                                                                                                                                                                                                                                                                    REFERENCE
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                                                                                                                                                                                                                                                                           /dev_stage="adult"
/lab_host="below [Life Technologies]"
/lab_host="below [Life Technologies]"
/lab_host="below [Life Technologies]"
/note="vector: pr773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco Ri; The UT-R-Al
library is a subtracted library derived from the UT-R-Al
library. The UT-R-Al library consisted of a mixture of
individually tagged normalized libraries constructed from
rat placenta, adult lung, brain, liver, kidney, heart,
spleen, ovary, and muscle. The tag is a string of 3-5
nucleotides present between the Not I site and the
oligo-dT track which allows identification of the library
of origin of a clone within the mixture: The subtracted
library (UI-R-Al) was constructed as follows: PCR
amplified cDNA inserts from a pool of approximately 3,840
UI-R-AO clones from which 3' ESTS had been derived was
used as a driver in a hybridization with the UI-R-AO
oligo-dr track served to identify it as a clone from the normalized adult Brain library. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics The following repetitive elements were found in this cDNA sequence: 1.35, >POLY_ABSimple_repeat
Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           converted to double-stranded circles and electroporated into DHIOB bacteria (Life Technologies) to generate the UI-R-Al library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       369 AGCGTCAGGCTTCACTGCATCATCCAGCTGCTGAAAGGGAGTCATCTCAAGACTCCCAGG 310
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Pred. No. 1.5e-22;
0; Mismatches 75;
                                                                                                                                                                                                 /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="Ur.R-Al-es-g-11-0-UI"
/clone_lib="UI-R-Al"
                                                                                                                                                                          organism="Rattus norvegicus"
                                                                                                                                 Location/Qualifiers
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109 c 1
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74.18;
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Best Local Similarity 74.1
Matches 274; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                            trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))

Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Ito, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H. Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shizaki, T., Sogabe, Y., Tominaga, N., Watanabe, S., Yagame, M., Tateno, M., Tomaru, Y., Yokohino, M., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muzamatsu, M., Okazaki, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                 Email: genome-resertc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                   Unpublished (1999)
On Feb 18, 1999 this sequence version replaced g1:4296972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="1110029c24"
/clone_lib="Mus musculus 18-day embryo C57BL/6J"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 150; DB 49;
Pred. No. 3.2e-19;
0; Mismatches 20;
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50 c 60 g 59
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/strain="C57BL/6J"
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89.4%;
                                                                                                                                                                                                                                                                                                                                                          Tel: 81-298-36-9145
Fax: 81-298-36-9098
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Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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AI071408/c
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/dev_stage="adult"
/lab_host="bellob (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/lote="Vector: pT7330-pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco Ri; The UI-R-C2
library is a subtracted library derived from the UI-R-C3
library, which is a subtracted library derived from the
UI-R-C3 library, The UI-R-C3 library consisted of a
mixture of individually tagged normalized libraries
constructed from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day
embryo. The tag is a string of 3-5 nuclectides present
between the Not I site and the oligo-dT track which allows
identification of the library of origin of a clone within
the mixture. The subtracted library (UI-R-C2) was
constructed as follows: PCR amplified cDNA inserts from
UI-R-C1 clones from which 3' ESTS had been derived was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence tag present in the CDNA between the NotI site and the oligo-dr track served to identify it as a clone from the normalized adult Lung library. CDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used as a driver in a hybridization with the UI.R-CI
library in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library) was
purified by hydroxyapatite column chromatography,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                          451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 9200
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               630 aggtectgccggctaaactctaaggataggccatcctcctgctggt-cagacctggagg 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 AGGICCIGCCGGCIAAACICIGAGGAIAGGCCAICCICCIGCIGGAIGCAGACCIGGAGG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   689 ctcacctgaattggagcccctctgtac---ctatctgggcaacaaagaaacctaccatga 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                             97044477
On Sep 12, 1996 this sequence version replaced gi:1404537
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Pred. No. 8e-17;
0; Mismatches 46; Indels 17;
                                                                                                                                                                                                                                         Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="UI-R-C2-nb-d-08-0-UI"
/clone_llb="UI-R-C2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Rattus norvegicus"
                                                                                                    Genome Res. 6 (9), 791-806 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="Sprague-Dawley/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: M13 Forward.
Location/Qualifiers
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Best Local Similarity 77.9%;
Matches 222; Conservative
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836 ttgcagggcctcccaacaatctctttaaataaataaaggagttgttc
                                                                                                                                                                                                                                    AA377893.1 GI:2030231
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                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Eutheria; Primates;
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EST90550 :
AA377893
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Matches 130;
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AA377893
                                                                                                                                                                          DEFINITION
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AUTHORS
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Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
                                                                                                                                                                                                                                                                                                                                                                                                                            Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Ito, M., Alzawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Haza, M., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H. Owa, C., Sato, K., Shibata, Y., Shiqemoto, Y., Shiraki, T., Sogabe, Y., Tominaga, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tomaru, Y., Yokhima, M., Watanabe, S., Yagame, M., Yamanura, T., Yokota, T., Yokhimo, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
                                                                                                                                                                                                     AV011309 167 bp mRNA EST 03-JUN-1999 AV011309 Mus musculus 18-day embryo C57BL/6J Mus musculus cDNA clone 1110031J03, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               716 ctatctgggcaacaaagaaacctaccatgaggctggggcacaatgagctccacaaaccac 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        776 agetttggtccacatgatggtcacacttggatataccccagtgtgggtaaggttggggta 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 ATGTACCCCAATATGGGTAGGGTTGGAGTAATGACAAGGGTTATGCAGGACCCTCCAAGA 46
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
On Jun 5, 1998 this sequence version replaced g1:3189141.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 135.8; DB 49; Length
Pred. No. 1.4e-16;
0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                                                                            /dev_stage="18-day embryo"
40 c 42 g 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090",
/clone="1110031J03"
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1. .167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Science Laboratory
806 atataccccagtgtgggtaaggttg
                                                                                                                                                                                                                                                                               94788296
AV011309.1 GI:4788296
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92.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 167)
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Best Local Similarity 92.2
Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Chie Owa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             further details.
                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                         house mouse
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AV011309
LOCUS
DEFINITION
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COMMENT
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Loases tto 247)

Sadams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.JT.,
Kelley, J.M., Kelley, J.C., Liul, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nquyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shifey, R.,
Badlarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hadson, P., Li, Y.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Melssner, P.S., Olsen, H.,
Raymond, L., Well, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Intial assessment of human gene diversity and expression patterns
                                                                                                                                                                                                                                       247 bp mRNA EST 21-APR-1997
Synovial sarcoma Homo sapiens cDNA 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: arkerlav@tigr.org

Email: arkerlav@tigr.org

Information eatalability, additional sequence and expression

Information related to this EST, please check the TIGR Human Gene

Index (http://www.iigr.org/tdb/hgi/hgi.html)

Seq primer: M13 Reverse.
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/dev_stage="adult, 20 yrs"
/note="Vector: pBluescript SR-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Mammalia;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Sep 12, 1996 this sequence version replaced gi:1404677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ï
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
882
                             121 TTGCAGGGCTCCCAAGAGTCTCTTTAAATAAATAAAGGAGTTGTTC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Pred. No. 2.2e-11;
0; Mismatches 23;
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Synovial sarcoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 t
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DEFINITION
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ORIGIN
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AUTHORS
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COMMENT
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AI074921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
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/lab_host="bhlob (life Technologies)"
/lab_host="bhlob"
/lab_host="bhlo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
Email: moscares@blue.weeg.ulowa.edu
The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the Noti Site and the oligo-dr track served to identify it as a clone from the normalized 18 day embryo library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Seg primer: M.3 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               library (UI-R-C3) was constructed as follows: PCRamplified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 234)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 origin of a clone within themixture. The subtracted
                                                                                                                                                 224 catactgctcgaaccttagtttccgcctgtacgaccagtggcgtgcttggatgcagaagt 283
Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AIS35068 234 bp mRNA EST 18-MAR-1999
UI-R-C3-sx-d-03-0-UI.S1 UI-R-C3 Rattus norvegicus CDNA clone
UI-R-C3-sx-d-03-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9704477
On May 18, 1998 this sequence version replaced g1:3136453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10116"
/clone="UI-R-C3-sx-d-03-0-UI"
/clone_lib="UI-R-C3"
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                                                                                                                                                                                                                                                                                                                 120 CGCACAAGACCNGNAACCAGCACAGGACGAGGGG 153
                                                                                                                                                                                                                                              284 cacacaagacccgaaaccaggtaggaaagttggg 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     discovery
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AI535068/c
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KEYWORDS
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TITLE
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cDNA inserts from UI-R-C2p clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UI-R-C2p library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hybroxypatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (LifeTechnologies) to generate the UI-R-C3 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996).
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              υχυναΠυΝ.sl Soares_senescent_fibroblasts_NbHSF Homo sapiens CDNA clone IMAGE:1664847 3', mRNA sequence.
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Email: (301) 496-1550
Email: Robert_Strausbergenih.gov
This clone is available royaity-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 761 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 367.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    683 tggaggotcacctgaattggagococtotgtac---ctatotgggcaacaaagaaaccta 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               740 ccatgaggctggggcacaatgagctcccacaaccacagctttggtccacatgatggtcac 799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 TGGAGGCTCACCTGAACTGGAGCCATCTGTACTGTCACTTTGGGGCAATGAAGAAACAA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Gaps
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Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 404)

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On Jan 17, 1998 this sequence version replaced gi:1900484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/map="17q21; between D17s1321 and D17s1325; xpl
between AFMA2127G1 and DX6745"
/clone="IMAGE:1664847"
/clone_11b="Soares_senescent_fibroblasts_NbHSF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 101; DB 47; Length 234;
Pred. No. 4.9e-10;
0; Mismatches 45; Indels 1
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/lab_host="DH10B (ampicillin resistant)"
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 74.0%;
Matches 174; Conservative 0
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AIO74921.1 GI:3401565
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RESULT 15
AA270365
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DEFINITION
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Washu HHMI Mouse EST Project
Washington University School of MedicineP
4444 Proset Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseestewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:239573
                                                                                                                                                                                                                                                                                                                     176 cggtggggggggggggtcaagcagttcctcggctggctcaagaagcacgcatactgctcga 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mel7b11.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:387741 5' similar to PIR:B38252 B38252 granulocyte colony-stimulating factor receptor precursor; mRNA sequence. W66776
                                                                                                                                                                                                                                                                                                                                      236 accttagtttccgcctgtacgaccagtggcgtgcttggatgcagaagtcacacaagaccc 295
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                    Score 100.2; DB 42; Length 404; Pred. No. 7.5e-10; 0; Mismatches 18; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Possible reversed clone: similarity on wrong strand
                                                                                                                                                                                         3 others
                                                                                                                                                                                                                                                                                    18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Marra M/Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence stop: 359.
Location/Qualifiers
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                                                                                                                                                                                                                                                   10.7%;
86.0%;
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W66776.1 GI:1375694
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                                                                                                                                                                                                                                                                                     Matches 111; Conservative
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                                                                                                                                                                                                                                                                    Similarity
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W66776/c
LOCUS
DEFINITION
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/note="Vector: pr7r3D-Pac (Pharmacia) with a modified boly1inker; Site_1: Not I: Site_2: Eco RI: 1st strand cDNA was primed with a Not I: -01190(dr) primer [5' refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined with a Not I refined wit
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[ (Dases 1 to 227)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T 3'), on equal amounts of mRNA from 2 13.5dpc and 2
State Univ., from 2 1; double-stranded by Minoru Ko, Wayne
State Univ., from 2 1; double-stranded cDNA was ligated th
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT/T3 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo.
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va63h12.rl Soares mouse 3NME12 5 Mus musculus cDNA clone
IMAGE:736103 5', mRNA sequence.
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WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                  embryo NbME13.5 14.5"
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Pred. No. 2.2e-08;
0; Mismatches 1;
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Seq primer: -28ml3 rev2 ET from Amersham
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Unpublished (1996)
clone-"IMAGE:387741"
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Best Local Similarity 98.9
Matches 93; Conservative
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3'), on total mouse RNA [provided by Minoru Ko, Wayne State Univ.]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "
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9.1%; Score 85; DB 30; Length 227;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
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Search completed: September 28, 1999, 15:38:13 Job time: 3281 sec

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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.	OM nucleic - nucleic search, using sw model	<pre>Run on: September 28, 1999, 16:39:42</pre>	Title: US-09-037-657-18 Perfect score: 834 Sequence: 1 cccacccttctcatcggctcatgggtcgaaaaggcggga 834		Genembl:* 1: 90_bal:* 3: 90_bal:* 4: 90_bal:* 5: 90_bal:* 6: 90_bal:* 7: 90_pli:* 9: 90_pli:* 10: 90_pri:* 11: 90_pri:* 11: 90_pri:* 12: 90_pri:* 13: 90_pri:* 14: 90_pri:* 15: 90_pri:* 16: 90_un:* 16: 90_un:* 17: 90_vi:* 18: em_fun:* 18: em_lin:* 23: em_lin:* 24: em_pl:* 25: em_pl:* 26: em_pl:* 27: em_pl:* 28: em_pl:* 29: em_lin:* 29: em_lin:* 21: em_lin:* 21: em_lin:* 22: em_lin:* 23: em_lin:* 24: em_pl:* 25: em_lin:* 26: em_pl:* 27: em_lin:* 28: em_lin:* 29: em_lin:* 39: em_lin:* 30: em_lin:* 31: em_lin:* 31: em_lin:* 32: em_lin:* 33: em_lin:* 34: em_lin:* 35: em_lin:* 36: 90_lin:* 37: em_lin:* 37: em_lin:* 38: em_lin:* 39: em_lin:* 30: em_lin:* 30: em_lin:* 30: em_lin:* 30: em_lin:* 30: em_lin:* 30: em_lin:* 40: em_lini:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.	SUMMARIES Result Query No. Score Match Length DB ID	1 834 100.0 834 5 A70388

07-MAY-1999

834

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A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING PATENT: WO 9811225-A 19-MAR-1998; NICOLA NICOS ANTONY (AU)
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Pred. No. 7e-181;
0; Mismatches 2;
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WO9811225.
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Location/Qualifiers
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Nicola, N. A., Fabri, L., F
Zhang, J., Alexander, W.,
Kikuchi, Y.
                                                1629 bp
from Patent
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ilarity 99.8%;
Conservative (
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                                                                                                            unidentified,
unidentified
unclassified.
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Matches 832; Conserv
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FLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKR
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Menoud, L. N., Mells, T. N. C., Kosco-Vilbols, M. H. and Gauchat, J. F. Cytokine Type-I Receptor Family

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quence presented
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623 c 525 g 273 t
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11arity 87.4%; Pred. No. 6.2e-143;
Conservative 0; Mismatches 105;
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/db_xref="taxon:9606"
/chromosome="19"
/man="10-"
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similar to the sequence
Number AC003112"
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230. .1384
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/gene="CLF-1"
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/gene="CLF-1"
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119. .1387
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Nicola, N.A., Fabri, L., Farley, A., Nash, A., Willson, T., Rakar, S.,
Zhang, J., Alexander, W., Hilton, D.J., Kojima, T., Maeda, M. and
Kikuchi, Y.
            GCTCTGGCCCTGGCCAACCTCAATGGGTCCAGGCAGGGGTCGGGGGACAACCTCGTGTGC 120
                                                                 268 aagcoctttaacatcagctgctggtcccggaacatgaaggatctcacgtgccgctggaca 327
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                                                                                                                                        181 AAACCCGTCAACATCAGCTGGTGGTCCAAGAACATGAAGGACTTGACCTGCCGCTGGACG
                                                                                                                                                                            328 ccgggtgcacacgggggagacattcttacataccaactactccctcaagtacaagtgagg
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Sequence 23 from Patent WO9811225.
A70393
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/db_xref="taxon:32644"
182 c 165 g 10
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SCRLAGLKRGTVYFVQVRCNPFGIYGSKKAGIMSEWSHPTAASTPRSERPGPGGGACE
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                                                                                                                                                                                                                                                 009
                                                                                                                                                              740 GAGATCIGGGIGGAGGCCACCACCGCCIGGGCTCTGCCCGCTCCGATGTACTCACGCTG 799
                                                                                              601 ggcctggaggaccagctgagtgtgcgctgggtctcaccaccagctctcaaggatttcctc 660
                                                                                                                                        919
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Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,Sahay,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and Kikuchi,Y.
                                541 gatgtcctggacgtggtgaccacggacccccaccgacgtgcacgtgacgctggttggg
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Pred. No. 9e-128;
0; Mismatches 92; Indels 0;
                                                                                                                                                                                                                                                                                              781 ttcgtccaagtgcgttgtaacccattcgggatctatgggtcgaaaaggcggg
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Sequence 24 from Patent WO9811225.
A70394
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/db_xref="PID:e1433703"
/db_xref="PID:94774673"
/db_xref="GI:4774673"
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:1. .1053
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87.7%;
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A70394.1 GI:4774672
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Best Local Similarity 87.7
Matches 654; Conservative
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Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar
Shang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
Kikuchi,Y.
                                                                                                                                                                                                                                                                                                        acactggatgtcctggacgtggtgaccacggacccccacccgacgtgcacgtggagccgc
                                           tccaggcagcagtcaggagacaatctggtgtgtcacgcccgagacggcagcattctggct
                                                     1 TCCAGGCAGCGGTCGGGGGACAACCTCGTGTGCCACGCCCGTGACGGCAGCATCCTGGCT
                                                                                                                                               AAGAACATGAAGGACTTGACCTGCCGCTGGACGCCCAGGGGCCCACGGGGACTTCCTC
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                                                                                                                                                                                    ccctatgagatctgggtggaagccaccaatcgcctaggctcaggatctgatgtcctc
                                                                                                                                                                                                                                                                                  Score 254.4; DB 5; Length 6663; Pred. No. 5.4e-49;
 Length 560;
                      65; Indels
54.7%; Score 456; DB 5; 88.4%; Pred. No. 4.7e-95;
                    0; Mismatches
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Sequence 28 from Patent WO9811225
A70398
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/db_xref="taxon:32644"
1852 c 1715 g 1634
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Query Match
Best Local Simi
Matches 495; (
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A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME PATENT: WO 9811225-A 19-MAR-1998; NICOLA NICOS ANTONY (AU)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6356 CCCACCTTCTCATCGGCTCCTCCCTGCAAGCTACCTGCTATACATGGAGACACACCT 6415
                                                                                                                                                                                                     ggggccaccgctgaggggctctactggaccctcaatggtcgccgcctgccctctgagctg 120
                                                             1 occaecetteteateggetectecetgeaagetacetgetetatacatggagacacacet 60
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Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Ra
Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M.
Kikuchi,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 30.5%; Score 254.4; DB 5; Length 11832; Best Local Similarity 99.6%; Pred. No. 5.2e-49; Matches 255; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                  ON Sequence 38 from Patent WO9811225.
1 A70408
94774683
A70408.1 GI:477/2
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/organism="unidentified"
/db_xref="taxon:32644"
a 3367 c 3298 g 272
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Location/Qualifiers
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us-09-037-657-18.rge

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repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Lij9NC03 R chromosome 19 cosmid library"
/note="Lij9NC03 cosmid library constructed at LLNL from
flow-sorted chromosomes from hybrid 5HL2-B, which carries
chromosome 19 as its only human chromosome."
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotta...

Eukaryotta...

Eukhoria: Primates; Catarrhini; Hominidae; Homo.

Lobases 1 to 40668)

Lamerdin.J.E., McCready,P.M., Adamson,A.W., Burkhart-Schultz,K.,

Gordon,L., Christensen,M., Kyle,A., Ramirez,M., Stilwagen,S.,

Kobayashi,A., Olsen,A.O. and Carrano,A.V.

Sequence analysis of an -1 Mb region containing the MEF2B gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           frame: 1, quality: good, score: 63.000"
complement(9629. .9672)
/note="predicted exon, program: grail2exons_human_1.3,
frame: 1, quality: excellent, score: 75.000"
/rpt_family=Alu"
10409. .10548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (21-NOV-1997) Human Genome Center, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
Location/Qualifiers
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: 1, quality: good, score: 62.000"
.8516
                                                                                          21-NOV-1997
                                                                       40668 bp DNA PRI 21-NOV-1997
from chromosome 19 specific cosmid R30292, genomic
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/cell_line="5HL2-B"
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9358. .935
Cmplemally-"LTR12"
Cmplement(9445. .9505)
/note-"predicted exon, pr
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complement(6486. .6772)
/rpt_family="Alu"
complement(7505. .7783)
/rpt_family="Alu"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="R30292"
                                                                                                                                                         sequence, complete sequence.
                                                                                                                                                                                                                                                           AC003112.1 GI:2636669
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Lamerdin, J.E.
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RESULT 10
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AUTHORS
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96% identity. --other overlapping matches: -(10435, .10548)
DDS similarity to AA136115 zk90b04.rl Scares pregnant
uterus NbHPU Homo saplens cDNA clone 490063 5'(1. 110);
33% identity. --(10466. 10548) DDS similarity to AA455628
zx33f04.rl Scares total fetus Nb2HF8 9w Homo sapiens cDNA
clone 788287 5'(1. 32); 95% identity. --(10486. 10548) DDS
similarity to AA009412 ze82h02.rl Scares fetal heart
NbHH19W Homo sapiens cDNA clone 365523 5'(1. 61); 97%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /noce-"DDS similarity to AA406406 zvlle07.sl Soares NhHMPU Sl Homo sapiens cDNA clone 75348 3' (1. .433); Score: 858 Indentity: 431/433 (998).---(14884. .15237) DDS similarity to W37175 zb21802.rl Soares fetal lung NbHL19W Homo sapiens cDNA clone 302666 5' (1. .355); 94%
                                                                                                                                                                                                                                                                                                                                                                                               complement(11869. .12161)
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2502. .12581
                                                                                                                                                                                                                                                                                                                                                                                         98% identity
                                                                                      identity.
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241 tgcctctatgttggc 255

07-MAY-1999

A/U386 938 bp DNA Sequence 16 from Patent WO9811225. A70386

RESULT 11 A70386 LOCUS DEFINITION ACCESSION

GI:4774665

94774665 A70386.1

unidentified. unidentified unclassified.

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

181

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identity.~~(15227. .14885) DDS similarity to AA121532
zk89c11.s1 Soares pregnant uterus NDHPU Homo sapiens cDNA
clone 490004 3' (342. .1); 99% identity.~~(1527. .14885)
DDS similarity to AA127694 zk89c11.r1 Soares pregnant
uterus NDHPU Homo sapiens cDNA clone 490004 5' (126. .467);
99% identity.~~(1527. .14897) DDS similarity to W46603
zc32hlo.r1 Soares senescent fibroblasts NDHSF Homo sapiens
cDNA clone 324067 5 (328. .1); 98%
identity.~~(1527. .15088) DDS similarity to W46604
zc32hlo.s1 Soares senescent fibroblasts NDHSF Homo sapiens
cDNA clone 324067 3' (322. .465); 96% identity."
15713. .15760
//note="DDS similarity to AA12153 zk89c11.s1 Soares
pregnant uterus NDHPU Homo sapiens cDNA clone 490004 3'
(389. .343); 99% identity.~~DDS similarity to AA127694
zk89c11.r1 Soares pregnant uterus NDHPU Homo sapiens cDNA
clone 490004 5' (77. .125); 99% identity.~(15735. .15713)
DDS similarity to W46603 zc32hlo.r1 Soares senescent
fibroblasts NDHSF Homo sapiens cDNA clone 324067 5'
(351. .329); 100% identity.~~(15735. .15713) DDS similarity
to W46604 zc32hlo.s1 Soares senescent fibroblasts NDHSF
Homo sapiens cDNA clone 324067 3' (299. .321); 100%
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A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME

/note="unnamed protein product"

/codon_start=1 /protein_id="CAB42574.1" /db_xref="PID:g4774666" /db_xref="PID:g4774666" /db_xref="GI:4774666"

Patent: WO 9811225-A 19-MAR-1998;
NICOLA NICOS ANTONY (AU)
LOCATION/QUALIFIERS
1. 938
//Organism="unidentified"
//db_xref="taxon:32644"

source

FEATURES

CDS

JOURNAL

TITLE

1 (bases 1 to 938)
Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S.,
Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and

/translation="GTVYFVOVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPG GGCDFRGGEPSGPVRRELKQFLGWLKKHAYCSNLSFRLYDOWRAWMOKSHKTRNOV GKLGBACVGGGEPERPDFGPOHTLLSKHRTRGSCPRADGVRREVRGSG" 1 245 c 272 g 178 t

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Length 938;

DB 5; L

7.9%; Score 66; DB 100.0%; Pred. No. 8.3

Query Match 7.9% Best Local Similarity 100.(Matches 66; Conservative

BASE COUNT

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769 ggcaccgtttacttcgtccaagtgcgttgtaacccattcgggatctatgggtcgaaaag 828
                                        1 GGCACCGTTTACTTCGTCCAAGTGCGTTGTAACCCATTCGGGATCTATGGGTCGAAAAAG 60
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Lagomorpha, Leporidae, Oryctolagus.

    (bases 1 to 2635)

                                                                                                                                                                                                                                                                                                             prolactin receptor.
Rabbit (14-day pregnant) mammary gland, cDNA to mRNA, clones
PRLR-2[1,4]............
                                                                                                                                                                                                  RABPRLR 2635 bp mRNA MAM
Rabbit prolactin receptor 2 mRNA, complete cds
J04510
                                                                                                                                                                                                                                                                                           GI:165669
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                                                                              829 gcggga 834
                                                                                                                     GCGGGA
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ACCESSION
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                                                                                                                                                                                                                                                                                                                                                   21408 GGAGCCACCGCCGAGGGCCTCTACTGGACCCTCAACGGGCGCCGCCTGCCCCTGAGCTC 21349
                                                                                                                                                                                                                                                                                                                                                                                            121 tcccgcctccttaacacctccaccctggccctggccctggctaaccttaatgggtccagg 180
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                         DB 11; Length 40668;
                                                                                                                                                       Query Match 24.1%; Score 200.6; DB 11; Length Best Local Similarity 86.7%; Pred. No. 9.8e-37; Matches 221; Conservative 0; Mismatches 34; Indels
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15-SEP-1989

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Local Similarity
           037273.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGFDTHLLEKGKSEELLSAFGCQDFPPTADCEDLLVEFLEVDDSEDQQLMPAHSKEHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPGMKPTDLDPDNDSGRGSCDSPSLLSEKCEEPQANPSTFHTPEVIEQPEKPKANVTH
TWDPQTISLVGKMPYLSVNGSKSSTWPLLQPGQHNTNSPYHNIADMCKLATSLDKIDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DALOSSKTTEAAGEEKATKOREVESSHSKAEQDTGWLLPKEKPPFISPKPLDYVEIHK
VNKDGALSLLLKOKENGDQTGKAGTPETSKEYAKVSRVMDNNILVLVQDPGAQNVALF
 Edery, M., Jolicoeur, C., Levi-Meyrueis, C., Dusanter-Fourt, I., Petridou, B., Bouturin, J.-M., Lesueur, L., Kelly, P.A. and Djiane, J. Identification and sequence analysis of a second form of prolactin receptor by molecular cloning of complementary DNA from rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                 CWWRPGADGGLPINYILIYHKEGETITHECPDYKTGGPNSCYFSKKHTSIWTIYIIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPESSIQIPNDFTMKDITVWIFVAVLSTIICLIMVWAVALKGYSMVTCIFPPVPGPKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
                                                                                           Proc. Natl. Acad. Sci. U.S.A. 86, 2112-2116 (1989)
9304578
Draft entry and computer-readable sequence for [1] kindly provided
by J.Djiane, 14-MAR-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aagctgaggtggtacggtcaggataacacatgtgaggagtaccacactgtggggccccac 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cococtgagaagccotttaacatcagctgotggtcocggaacatgaaggatctcacgtgc 318
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                                                                                                                                                                                                                                                           'note-"prolactin receptor 2 signal peptide"
                                                                                                                                                                                                                                                                                                'note="prolactin receptor 2 precursor"
                                                                                                                                                                                       /organism="Oryctolagus cuniculus"
/db_xref="taxon:9986"
477. .548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="prolactin receptor
668 c 603 g 647
                                                                                                                                                                                                                                                                                                                                       Protein_id="AAA31457.1"
db_xref="PID:g165670"
db_xref="G1:165670"
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bp upstream of BamHI site.
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VYPTSGQPSGYSAACSGALDTSGSYHCSMRAMSLYSGERPGHKCVPPRALEEGLAEHP
TGAPSRLGALSLPSGQEGALGAGHPHGGTAAGQPAASWYLNHGAELSHLPGHTYGSQQ
QTFPNVREMFTSHRLGMESEHQVSSNSACQIPYRSAPSLYRHTAPYSYDCTKY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DDKKPGKGSYWTLDPDSYNMFENGSFLRRRRRFKKKDVSKEMEEARERLLKEQPKPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MGNPMSVYSGHAEQYAAGMGRSYGPYHPHQPAAPKDLVKPPYSY
                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (29-SEP-1995) Bettina S. Freyaldenhoven, Department of Molecular and Experimental Medicine, SBR-7, Scripps Research Institute, 10666 North Torrey Pines Road, La Jolla, CA 92037, USA Location/Qualifiers
                                                                                                         Aves; Neognathae; Calliformes; Phasiahidae; Phasianinae; Gallus. [ [ Dases 1 to 1531]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     630 ggtctcaccaccagctctcaaggatttcctttccaagccaagtaccagatccgctaccg 689
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                                                                                                                                                                                                               Aberrant cell growth induced by avian winged helix proteins Cancer Res. 57 (1), 123-129 (1997)
                                                                                                                                                                   1 (bases 1 to 1531)
Freyaldenhoven, B.S., Freyaldenhoven, M.P., Iacovon1, J.S. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143. .1480
/note="winged helix transcription factor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="winged helix protein CWH-2"
/protein_id="AAC60065.1"
                                                                                                                                                                                                                                                                                                                           Freyaldenhoven, B.S. and Freyaldenhoven, M.P. Direct Submission
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Pred. No. 1.2;
0; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Gallus gallus"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="PID:g1766075"
/db_xref="G1:1766075"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'tissue_type="embryo"
                                                                                 Gallus gallus
Eukaryota; Metazoa; Chordata;
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al Similarity 50.7%;
104; Conservative
GI:1766074
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FSVRNIWTLRTSAGDLSPVSAASGRTGTGMELVYPTSGOPSGYSAACSQALDDSGSYH
CSNRAMSLISGERPGHMCVPPAALEEGLAEHPTGAPSPRGPOPAVGAGGSAGGRAPAR
RHCAGOPAASWYLNGAELSHLPGHTFGSQQQTFPNVREMFTSHRLGMESEHQVSSNS
APSLYRHTAPYSYDCTKY"
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FLRRRRRFKKKDVSKEKEEARERLLKEQPRPPGLPGADLPKEASSSSSSSSSSKVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MQARYSVSDPNALGVVPYLSEQNYYRTAGTYGGMGNPMSVYSGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEQYAAGMGRSYGPYHPHQPAAPKDLVKPPYSYIALITMAIQNAPDKKITLNGIYQF:
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Columba livia
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Aves; Neognathae; Columbiformes; Columbidae; Columba.
1 (bases 1 to 2713)
Chen,X. and Horseman,N.D.
                                                                                                                                                                                             Direct Submission
Submitted (28-MAR-1997) Molcular Immunology, School of Medicine,
Chiha University, 1-8-1, Inohana, Chuo-ku, Chiba 20, Japan
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   750 tetegegggeetgaageeeggeacegtttaettegteeaagtgegttgtaaceeattegg 809
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Columba livia prolactin receptor mRNA, complete cds.
U07694
                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                           /product="winged helix transcriptional factor MFH-1"
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                                                                    Arase,Y., Koseki,H. and Miura,N.
Winged helix transcriptional factor MFH-1 is required for
generation of medial structures of the vertebrae and the
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/note-"mesenchymal forkhead homolog-1"
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Pred. No. 1.2;
0; Mismatches 101;
               Sukaryota; Metazoa; Chordata; Craniata;
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                                                                                                                                                                                                                                                                                /organism="Gallus gallus"
/db_xref="taxon:9031"
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Best Local Similarity 50.7%;
Matches 104; Conservative
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SLICLYMSWTMVLKGYRMIAFILPPVPGPKIKGIDTHLLETGKSEELLSALGCHGFPP
TSDCEELLIEYLEVEDSEDQQLMPSHDNGHPSKNAKMIAKETDSDSGRGSCDSPSLLS
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                                                                                                                                                                                                                                                                                                                                                                                                                             /clone-"pCLLR.
/clone_lib-"assembled from a clone of pigeon crop lambda
gtll cDNA library and a PCR product"
/tissue_type-"crop"
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                                                                                                                                                                                                            Submitted (14-MAR-1994) Xiaojuan Chen, Physiology & Biophysics, University of Cincinnati Medical College, 231 Bethsda Ave., Cincinnati, OH 45267, USA Location/Qualifiers
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expression, and mutational analysis of the pigeon
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/protein_id="AAAA20646.1"
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                            prolactin receptor
Endocrinology 135 (1), 269-276 (1994)
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Search completed: September 28, 1999, 16:39:55 Job time: 6982 sec

us-09-037-657-18.rng

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

September 28, 1999, 16:45:44; Search time 303.81 Seconds (without alignments) 686.811 Million cell updates/sec Run on:

US-09-037-657-18 834

Title: Perfect score: Sequence:

1 occaccottotcatoggoto.....atgggtogaaaaggoggga 834

IDENTITY_NUC Scoring table: 311585 seqs, 125096042 residues Searched:

N_Geneseq_36:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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PF	11-	11-SEP-1997;	997;	G02479.	. 6										
д а	11-5	SEP-19	, , 966	AU-00	AU-002246.										
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S C	Cla	Claim 7; Page	Page	93-9	93-95; 182pp; English.	, dd;	Eng1	ish.							
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NR6.1 gene.
proliferation; cell differentiation; can
neuronal proliferation; drug screening;
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V27140;
29-SEP-1998 (first entry)
Novel haemopoietin receptor Ni
Haemopoietin receptor in
Haemopoietin receptor in
cell survival; therapeutic; ne
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ilarity 99.8%;
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Name J.

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Name J.

New isolated haemopoietin receptor - used for developing products

To includating proliferation, differentiation and survival of cells,

e.g. neuronal cells

Example 8; page 99-100; 183pp; English.

NR 6 is a novel haemopoietin receptor (HR). Interaction between the novel

HR and a ligand facilitates proliferation, differentiation and survival.

Cof a wide variety of cells: The HR and it's derivatives can be used for

modulating the activity of the receptors e.g. to requiate development,

maintenance or regeneration in an array of different cells and tissues in

vitro and in vivo. They can be present in therapeutics used for

modulating neuronal proliferation, differentiation and survival. The

condulating neuronal proliferation, differentiation and survival. The

condulating neuronal proliferation and survival. The

conducts can also be used for detection and diagnosis, e.g. for cancers

or predisposition to cancers, or for drug screening.

Sequence 1930 BP; 375 A; 623 C; 561 G; 371 T;
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11-SEP-1997; G02479.
11-SEP-1995, AU-002246.
(AMRA-) AMRAD OPERATIONS PTY LTD.
(DZIEZ) DZIEGLEWSKA H E.
Alexander N. Parley A, Hilton DJ, Kikuchi Y, Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
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LO V27158
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DT 29-SEP-1998 (first entry)
E Gnepliced murine NR6 nucleotic
E Haemopoletin receptor: cell pi
KW MOUSE.
NW 90811225-A2.
PN W09811225-A2.
PN WNR-1997; G02479.
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v27141;
29-SEP-1998 (first entry)
Novel haemopoietin receptor NR6.2 gene.
Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
cell survival; therapeutic; neuronal proliferation; drug screening; ss;
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P-PSDB; W55012.
New isolated haemopoletin receptor - used for developing products
for modulating proliferation, differentiation and survival of cells,
      gatgacgtcagcaaccagacctcctgccgtctcgcgggcctgaagcccgggcaccgtttac
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(DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Kolima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson.
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99.8%; Pred. No. 3.2e-208;
ative 0; Mismatches 2;
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1. .1278
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llarity 99.8%; Pred. No. 3.2e-208;
Conservative 0; Mismatches 2; Indels 0;
/*tag= a
/product= "Haemopoietin receptor NR6.1"
                                                                         (DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
                                                               AMRA-) AMRAD OPERATIONS PTY LTD DZIE/) DZIEGLEWSKA H E.
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11-SEP-1996; AU-002246.
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98-260970/23.
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V41688.
C5-OCT-1998 (first entry)
Nucleotide sequence of the murine U4 gene.
Murine; U4 protein; haematopojectin receptor superfamily;
cell proliferation; immune response; antibody; cell differentiation; autoimmune disease; cancer; allergy; ds.
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122. .1399
/*tag= a
/product= "U4 protein
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the haematopoietin receptor superfamily, used in the method of the invention for the modulation of cell proliferation, or the immune response. Transformed mammalian cells are used to produce recombinant U4 protein. The U4 protein is used to screen for specific binding agents, raise antibodies. It is also used as reagents for assays and as tissue markers for isolation of compate ligands and receptors, and in pharmaceutical compositions which may modulate cell proliferation, cell differentiation, and the immune system (e.g. for treating immune deficiency, inherited or the result of infection, autoimmune diseases, sequence 1656 BP; 318 A; 552 C; 478 G; 308 T;
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5.7e-207;
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The present sequence encodes a protein designated Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-l on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-l in the blood, and to discover other possible Zcytor5 ligands. A probe and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the therapeutically to modify Zcytor5 ligand effects.

Sequence 1724 BP; 350 A; 550 C; 500 G; 324 T;
                                                                               growth factor;
s; cardiotrophin-1;
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                                           17-MAR-1999 (first entry)

CDNA encoding rat 2cytor5.

CSCYLOT5: cytckinin-like receptor; down-regulation; growth
maintenance factor; thyroid; heart; skeletal muscle; card
cardiac pathology; heart enlargement; 2cytor5 ligand; ss.

Rattus sp.
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TE;
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                                                                                                                        Location/Qualifiers
159. .1436
/*tag= a
/product= 2cytor5
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01-MAY-1997; US-045287.
01-MAY-1997; US-05030.
12 FEB-1998; US-023890.
(ZYMO) ZYMOGENETICS INC.
Adams RL, FOSter DC, Gilbert T,
LOK S, Presnell SR, Whitmore TE
                         V70896 standard; cDNA; 1724 BP. V70896;
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Best Local Similarity 94.5
Matches 788; Conservative
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P-PSDB; W70862
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Disciosure, Page 68-70; 55pp; English.

The present sequence encodes an allelic varaint of protein designated 2cytors, which is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the
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CDNA encoding an allelic varaint of human 2cytor5.

Zcytor5, cytokinin-11ke receptor; down-regulation; growth factor; maintenance factor; thyroid; heart; skeletal. muscle; cardiotrophin-1; cardiac pathology; heart enlargement; Zcytor5 ligand; allelic varaint;
New mammallan cytokinin-like receptor Zcytor5 - useful for, e.g. down_regulating Zcytor5 natural ligands or detecting cardiotrophin-1
                                                                                                                                                                                            cacactgtggggccccactcatgccatatccccaaggacctggccctcttcactccctat
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SR, Whitmore TE;
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88. .1365
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/product= 2cytor5
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01-MAY-1997; US-850030.
13-FEB-1998; US-023890.
(ZYMO) ZYMOGENETICS INC.
Adams RL, FOSTEN DC, Gilbe
LOK S, PRESNELL SR, Whitm
WPI; 99-034662/03.
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e used to purify Z.
15 ligand effects.
604 C:
                                    Score 666.6; DB 1;
Pred. No. 2.6e-165;
0; Mismatches 104;
           modify Zcytor5
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     could
                                   79.9%;
ilarity 87.5%;
Conservative
      antibody
           to
BP;
                                    Query Match
Best Local Similarity
Matches 729; Conserv
           therapeutically
Sequence 1813
     anti-idiotypic
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V41689 standard; cDNA; 1579 BP.
V41689;
26-OCT-1998 (first entry)
Nucleoride sequence of the human U4 gene.
Human; U4 protein; haematopoietin receptor superfamily;

Human;

38483

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New nucleic acid encoding U4 haematopoietin receptor superfamily chain - potentially useful, e.g. for modulating cell proliferation or immune response, for treating cancer and auto:immune disease claim 1; Page 28; 38pp; English.

Claim 1; Page 28; 38pp; English.

Chis is the nucleotide sequence encoding the human U4 protein from the haematopoietin receptor superfamily, used in the method of the invention for the modulation of cell proliferation, or the immune response. Transformed mammalian cells are used to produce recombinant U4 protein. The U4 protein is used to screen for specific binding agents, raise antibodies. It is also used as reagents for assays and in pharmaceutical compositions which may modulate cell proliferation, cell differentiation, and the immune system (e.g. for treating immune deficiency, inherited or the result of infection, autoimmune diseases, sequence 1579 BP; 304 A; 535 C; 473 G; 257 T;
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cell proliferation; immune response; antibody; cell differentiation; autoimmune disease; cancer; allergy; ds.
Homo sapiens.
Location/Qualifiers
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Pred. No. 6.7e-165;
0; Mismatches 105; Indels
                                                                                                                                 protein'
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15-JAN-1998.
16-JAN-1997. US-784863.
(GEMY ) GENETICS INST INC.
COllins M, Donaldson DD, Neben T,
WPI: 98-414109/35.
P-PSDB: W59805.
                                                                                                                               "U4
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Best Local Similarity 87.4%;
Matches 728; Conservative
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CDNA encoding human Zcytor5.

2cytor5; cytokinin-like receptor; down-regulation; growth factor;
maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
cardiac pathology; heart enlargement; 2cytor5 ligand; ss.
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The present sequence encodes a protein designated Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe and integrity of the Zcytor5 gene on chromosome 19. Antibodies and therapeutically to modify Zcytor5 ligand effects.

Sequence 1690 BP; 319 A; 592 C; 505 G; 274 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             non-memmanian cytokinin-like receptor Zcytor5 - useful for, e.g. down-regulating Zcytor5 natural ligands or detecting cardiotrophin-l in blood
                                                                                                                                          gatgtcctggacgtggtgaccacgacgacccccaccgacgtgcacgtgagccgcgttggg
                                             99cctggaggaccagctgagtgtgcgctgggtctcaccaccagctctcaaggatttcctc
                                                                                                                 761 TITCAAGCCAAATACCAGATCCGCTACCGAGTGGAGGACAGTGTGGACTGGAAGGTGGTG
                                                                                                                                                                                         79.7%; Score 665; DB 1; Length 1690; B7.4%; Pred. No. 6.8e-165; Conservative 0; Mismatches 105; Indels
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Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner Lok S, Presnell SR, Whitmore TE;
WPI; 99-034662/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New mammallan cytokinin-like receptor 2cytor5
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                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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/product= 2cytor5
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01-MAY-1997; US-045287.
01-MAX-1997; US-850030.
13-FEB-1998; US-023890.
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Best Local Similarity
Matches 728; Conserv
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P-PSDB; W70860
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05-NOV-1998.
01-MAY-1998; U
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29-SEP-1998 (first entry)
Nucleotide sequence of clone HFK-66 encoding human NR6.
Haemopoietin receptor; cell proliferation; cell differentiation; can
cell survival; therapeutic; neuronal proliferation; drug screening;
                                     tocogoctcottaacacotcoaccotggccctggccctggctaaccttaatgggtccagg
                                               tgcctctatgttggcttgcccctgagaagccctttaacatcagctgctggtcccggaac
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                                                                           781 ttcgtccaagtgcgttgtaacccattcgggatctatgggtcgaaaaggcggg
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ID V27144 standard; cDNA; 1391 BP
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11-SEP-1996; AU-002246.
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                                                      claim 7; Page 102-104; 182pp; English.

The NRG gene encodes a novel Haemopoietin receptor (HR). Interaction between the novel HR and a lighand facilitates proliferation,

differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or of rary screening.

Sequence 1391 BP; 281 A; 459 C; 417 G; 234 T; screening.
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and survival of cel
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lton DJ, Kikuchi Y,
NA, Rakar S, Willson
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Pred. No. 1.3e-147;
); Mismatches 92;
                               P-PSDB; W55015.
New isolated haemopoietin receptor - used for
for modulating proliferation, differentiation
L, Farley A, Hilton
Nash A, Nicola NA, R
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Best Local Similarity 87.7%;
Matches 654; Conservative
   Alexander W, Fabri
Kojima T, Maeda M,
                         98-260970/23.
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While 90-260970/23.

While 90-260970/23.

New isolated haemopoletin receptor - used for developing products for modulating proliferation, differentiation and survival of cells.

For modulating proliferation, differentiation and survival of circles. Present the movel haemopoletin receptor (HR). Interaction between the novel NR6 is a novel haemopoletin receptor (HR). Interaction between the novel NR6 is a novel haemopoletin receptor (HR). Interaction and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors of ifferentiation and survival maintenance or regeneration in an array of different cells and tissues in control in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.
                                                                                                                                               V27159;
29-SEP-1998 (first entry)
PCR product for human NR6.
Haemopoletin receptor; cell proliferation; cell differentiation; cancer
cell survival; therapeutic; neuronal proliferation; drug screening; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; · Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cggaacatgaaggatctcacgtgccgctggacaccgggtgcacacgggggagacattctta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 560;
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                                                                                                                                                                                                                                                                 Homo sapiens.

WO9811225-A2.
119-MAR-1998.
11-SEP-1995; G02479.
11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS PTY LTD.
(DZIEC/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Rojana T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
Shang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.7%; Score 456; DB 1; L
88.4%; Pred. No. 2.1e-110;
ive 0; Mismatches 65;
833
                  gggatctatgggtcgaaaaaggcggg
                                                                                                                                   BP.
                                                                                                                                 standard; DNA; 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         al Similarity 88.4
495; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S:
Matches 495;
                                                                                                                                   V27159
                                                                                                                                                                                                                                                         Нишап.
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novel

V27145 standard; DNA; 6663 BP

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T for modulating releases

T e.g. neutonal calls

Claim 9; Fig 3; 182pp; English.

Claim 9; Fig 3; 182pp; English.

C between the novel HR and a ligand facilitates proliferation,

differentiation and survival of a wide variety of cells. The HR and it's

C derivatives can be used for modulating the activity of the receptors e.g.

CC different cells and tissues in vitro and in vivo. They can be present in

CC therapeutics used for modulating neuronal proliferation, differentiation

CC therapeutics used for modulating neuronal proliferation, differentiation

CC and survival. The products can also be used for detection and diagnosis,

CC e.g. for cancers or predisposition to cancers, or for drug screening.
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                                                                                                                                                                                                                                                           29-SEP-1998 (first entry)
Nuclectide sequence for murine NR6 containing additional 5N sequence.
Haemopoletin receptor; cell proliferation; cell differentiation; cancer; cell survival; therapeutic; neuronal proliferation; drug screening; ss;
                   6416 GGGGCCACCGCTGAGGGCTCTACTGGACCTTCAATGGTCGCCGCCTGCCCTGAGCTG 6475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9999ccaccgctgaggggctctactggaccctcaatggtcgccgcctgccctctgagctg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI: 98-260970/23.
New isolated haemopoietin receptor - used for developing products
for modulating proliferation, differentiation and survival of cells,
595 gttgggggcctggaggaccagctgagtgtgcgctgggtctcaccaccagctctcaaggat
                                                         655 ttcctcttccaagccaagtaccagatccgctaccgcgtggaggacagcgtggactggaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 254.4; .DB 1; Length 11832;
Pred. No. 2.3e-57;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                              (DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
                                                                                                                                                                                                                                                                                                                                                                                                                    (AMRA-) AMRAD OPERATIONS PTY LTD (DZIE/) DZIEGLEWSKA H E.
                                                                                                                           gtggtggatgacgtcagcaa 734
                                                                                                                                                    541 GTGGTGGACGATGTGAGCAA 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 255; Conservative
                                                                                                                                                                                                                                                                                                                                                                        19-MAR-1998.
11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                           Mus sp.
WO9811225-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local
                                                                                                                        715
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Claim 8; Page 108-114; 182pp; English.

Claim 8 Page 108-114; 182pp; English.

The NR6 gene encodes a novel Haemopoletin receptor (HR). Interaction between the novel HR and a ligand facilitetes proliferation, differentiation and survival of a wide variety of cells. The HR and it's products can be used for modulating the activity of the receptors e.g. to requiste development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.

Sequence 6663 BP; 1462 A; 1852 C; 1715 G; 1634 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1185 CCACCCTTCTCATCGCTCCTCCTCCTCCAAGCTACCTGTATACATGAGAGACACCCT 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 cccaccttctcatcggctcctccctgcaagctacctgctctatacatggagacacact 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; W55016.
New isolated haemopoletin receptor - used for developing products
for modulating proliferation, differentiation and survival of cells,
                                                     Mucrecide sequence of Murine NR6.
Haemopoletin receptor; cell proliferation; cell differentiation; cancer; cell survival; therapeutic; neuronal proliferation; drug; Screening; SS; Mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tocogoctcottaacacctccaccctggccctggccctggctaaccttaatgggtccagg
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                                                                                                                                                                                                                                                                                                                                                                                                 19-MAR-1998.
11-SEP-1997; GD2479.
11-SEP-1996; AU-002246.
(AMRA-) ANRAD OPERATIONS PTY LTD.
(DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
                                                                                                                                                                                                                                                                                                                                              /note= "No start or stop codon given'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 254.4; DB 1;
Pred. No. 2e-57;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                               /product- "Murine NR6"
                                                                                                                                                                                                                      Location/Qualifiers
1182. .1744
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                     3 (first entry)
sequence of Murine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.5%;
99.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 99.6
Matches 255; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tgcctctatgttggct 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J;
98-260970/23.
      V27145;
02-0CT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhang
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V70897
ID V70897
AC V70897;
DT 17-MAR-
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NAME OF COLOR OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF
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WPI: 99-034662/03.
New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
down-regulating Zcytor5 natural ligands or detecting cardiotrophin-l
in blood

Example 1; Page 77; 55pp; English.

RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM, Presnell SR, Whitmore TE;

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The present sequence represents an expressed sequence tag (EST) used to identify CDNA encoding a protein designated Zcytor5, which is a cytoKinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-l on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-l in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcytor5 and therapeutically to modify Zcytor5 ligand effects.
Sequence 259 BP; 64 C; 81 G; 46 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          710 ggaaggtggtggatgacgtcagcaaccagacctcctgccgtctcgcgggcctgaagcccg 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GGAAGGTGGTGGANGATGTGAGCAACCAGACCTTCTGCCG-CTGGNCGGCCTGAAACCCG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 GCANCGTGTACTTCGTGCAAGTGCGCTGCAANCCCTTTGGCATCTATGGCTNCAAGAAAG 179
           zcytor5; cytokinin-like receptor; down-regulation; growth factor;
maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-l;
cardiac pathology; heart enlargement; zcytor5 ligand; EST; ss.
W09849307-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                  New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g. down-regulating Zcytor5 natural ligands or detecting cardiotrophin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    770 gcaccgtttacttcgtccaagtgcgttgtaacccattcgggatctatgggtcgaaaaagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.4%; Score 128.8; DB 1; Length 259; ilarity 83.2%; Pred. No. 5.3e-25; Conservative 0; Mismatches 30; Indels 1
                                                                                                                                                                                                                                                (ZYMO) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
LOK S, Presnell SR, Whitmore TE;
WPI; 99-034662/03.
Expressed sequence tag used to identify human Zcytor5.
                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 77; 55pp;
                                                                                                                                                                                  01-MAY-1997; US-045287
01-MAY-1997; US-850030
13-FEB-1998; US-023890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 153; Conser
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                                                                                                                                                    The present sequence represents an expressed sequence tag (EST) used to identify cDNA encoding a protein designated zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify zcytor5 and therapeutically to modify Zcytor5 ligand effects.
Sequence 210 BP; 31 A; 84 C; 57 G; 34 T;
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9.7%; Score 81.2; DB 1;
Best Local Similarity 83.6%; Pred. No. 1.4e-12;
Matches 92; Conservative 0; Mismatches 18;
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Search completed: September 28, 1999, 16:45:58 Job time: 7343 sec

17-MAR-1999 (first entry)

Expressed sequence tag used to identify human Zcytor5.

Zcytor5; cytokinin-like receptor; down-regulation; growth factor; maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-l; cardiac pathology; heart enlargement; Zcytor5 ligand; EST; ss. WO9849307-A1.

RESULT 15 V70899

US-074721. US-045287. US-850030. US-023890.

13-FEB-1998; C 01-MAY-1997; U 01-MAY-1997; U

05-NOV-1998. 01-MAY-1998; U08865

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38
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Sequence 109, App
                                                                                                  5; Search time 152.56 Seconds (without alignments) 501.168 Million cell updates/sec
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/cgn2_6/ptcdata/2/ina/5B_COMB.seq:*
/cgn2_6/ptcdata/2/ina/5D_COMB.seq:*
/cgn2_6/ptcdata/2/ina/5D_COMB.seq:*
/cgn2_6/ptcdata/2/ina/FCTUS9_COMB.seq:*
/cgn2_6/ptcdata/2/ina/FCTUS9_COMB.seq:*
          GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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                                                                                                                                                                                                                                                    176461 seqs, 45838279 residues
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                                                                                                  September 28, 1999, 16:40:05
                                                                   OM nucleic - nucleic search, using sw model
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Sequence:
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66666666		4,1	SELUTION SELUSOR SELUSOR APPLICANT: DORNE APPLICANT: SCHEI	APPLICANT: FAI TITLE OF INVENT NUMBER OF SEQUI	ADDRESSEE STREET: CITY: Al	~ ``	MEDIUM TY	OPERATING SOFTWARE:	CURRENT APPLICATION DATA: APPLICATION NUMBER: US	FILING DATE: CLASSIFICATION: IOR APPLICATION	APPLICATION NUMBER: FILING DATE:			REFERENCE/DOCKET TELECOMMUNICATION		FORMATION FOR SEQ ID NO SEQUENCE CHARACTERISTIC	LENGTH: 7218 TYPE: nucle1 STRANDEDNESS:		7	511	4;	<pre>cccaccttctcatcggctcctccagctacctgctctatacatggagacacct :::</pre>	ggggccaccgctgaggggctctactggaccctcaatggtcgccgcctgccctctgagctg
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LOCATION: 222.425
OTHER INFORMATION: frame"
OTHER INFORMATION: frame"
NAME/KEY:
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NAME/KEY:
LOCATION: 451..747
OTHER INFORMATION: frame"
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Little, Michael C.
APPLICANT: Beyer Jr., Mayne F.
TITLE OF INVENTION: MYCOBACTERIOPHAGE SPECIFIC FOR THE
TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS COMPLEX
NUMBER OF SEQUENCES:
GORRESPONDENCE ADDRESS:
ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
ADDRESSEE: Company
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LOCATION: 747..1109
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/402,282
                                                                                                                                                                                                                                         Sequence 3, Application US/08402282
Patent No. 5476768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FUGIt, Donna R.
REGISTRATION NUMBER: 32,13
REFERENCE/DOCKET NUMBER: P
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1564 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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LOCATION: 1109..2014
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1 Becton Drive
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Huang Ph.D, Wai Mun
TITLE OF INVENTION: Method and Compositions for
TITLE OF INVENTION: Identification of Species in a Sample
NUMBER OF SEQUENCES: 207
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35.4; DB 2;
Pred. No. 0.58;
0; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Trask, Britt and Rossa STREET: P.O. Box 2550
CITY: Salt Lake City
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 109, Application US/08470179 Patent No. 5645994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Actinomyces naesundii
US-08-470-179-109
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ATTORNEY/AGENT INFORMATION:
NAME: Swelgert Ph.D. Susan E.
REGISTRATION NUMBER: 36,289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 54.1%;
Matches 72; Conservative
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nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 801-531-9168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                          NAME/KEY: misc_feature
LOCATION: 2747.3109
OTHER INFORMATION: /function- "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 3109.3444
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 3731.4855
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
OTHER INFORMATION: /function- "potential open reading OTHER INFORMATION: frame"
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LOCATION: 5382..5747
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OTHER INFORMATION: frame"
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LOCATION: 3444.3728
OCHER INFORMATION: /function- "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 5837.6307
OTHER INFORMATION: /function= "potential open reading
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LOCATION: 6403..7770
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OTHER INFORMATION: frame"
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LOCATION: 7770..8006
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 8033.8236
OTHER INFORMATION: /function=."potential open reading
OTHER INFORMATION: frame"
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LOCATION: 8244..9443
OTHER INFORMATION: /function= "potential open reading
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LOCATION: 9450..1024
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LOCATION: 10371..10586
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 4855..5376
OTHER INFORMATION: /function= "potential coding
OTHER INFORMATION: sequence"
OTHER: INFORMATION: /product= "L5 gp37 homolog".
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LOCATION: 11115..11786
OTHER INFORMATION: /fur
OTHER INFORMATION: fran
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Db 12218 TCGGCAAGCACCGGCGGCTGTTCGATGACCGGCCGAACACGGTAGCGCTTACCGAGGCCC 12277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12338 ACCAGGACGACGACGACGACGCCCGTGCAGTCCCTCGGCGACGAGCACCGCCCCC 12395
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APPLICANT: Handlich, Paul T.
APPLICANT: Handlich, Michael C.
APPLICANT: Beyer Jr., Wayne F.
ITLE OF INVENTION: MYCOBACTERIOPHAGE SPECIFIC FOR THE TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS COMPLEX NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS: 6 COMPLEX ADDRESSEE: Richard J. Rodrick, Becton Dickinson and STREET: 1 Becton Drive CITY: Franklin Lakes
STREET: NJ
COUNTRY: US
                                                                FEATURE:
NAME/KET: misc_feature
LOCATION: 12748...14499
OTHER INFORMATION: function= "potential open reading
OTHER INFORMATION: frame"
FEATURE:
NAME/KET: misc_feature
LOCATION: 14771...15154
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 15664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
LOCATION: 11917..12741
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function- "potential open reading frame"
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frame"
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APPLICATION NUMBER: US/08/508,004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
4.1%; Score 34; DB 1;
Best Local Similarity 49.4%; Pred. No. 3.8;
Matches 88; Conservative 0; Mismatches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 07417
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: 15154..15426
OTHER INFORMATION: /fun
OTHER INFORMATION: fram
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NAME/KEY: misc_feature
LOCATION: 3444.3728
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 2747..3109
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 5382..5747
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 2034..2747
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 3109.3444
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 3731.4855
OCHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 451..747
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OTHER INFORMATION: frame"
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LOCATION: 747..1109
OTHER INFORMATION: /function="potential open reading
OTHER INFORMATION: frame"
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LOCATION: 222.425
OCHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 1109..2014
OCHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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sequence"
/product= "L5 gp37 homolog"
                                            RRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/402,282
FILING DATE: 10-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                  NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-1
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                       LENGTH: 1564 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 4855.5376
OTHER INFORMATION: /func
OTHER INFORMATION: /prod
27-JUL-1995
1: 435
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COCATION: 5337.05

OTHER INFORMATION: (function - potential open reading of the intervention) (function - potential open reading other information: frame - partial recomments and the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information of information
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Score 34; DB 1; Length 15664; Pred. No. 3.8; 0; Mismatches 90; Indels

Query Match
Best Local Similarity 49.4%;
Matches 88; Conservative

449 tececaaggacetggeeetetteactecetatgagatetgggtggaagceaceaategee 508

us-09-037-657-18.rni

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OTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame" | FPATURE: NAME/KEY: misc_feature
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NAME/KEY: misc_feature
LOCATION: 5837..6307
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
NAME/KEY: misc_feature
LOCATION: 6403..7770
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 3109..3444
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: 'frame"
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LOCATION: 3731..4855
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 5382..5747
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 8033..8236
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 "potential open reading
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LOCATION: 8244..9443
OTHER INFORMATION: /function- "potential open reading
OTHER INFORMATION: frame"
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frame"
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OTHER INFORMATION: /function- "potential open reading OTHER INFORMATION: frame"
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OTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame"
EATURE:
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OTHER INFORMATION: /function= "potential coding OTHER INFORMATION: sequence"
OTHER INFORMATION: /product= "L5 gp37 homolog"
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LOCATION: 2747..3109
LOCATEN INFORMATION: /function="potential open
OTHER INFORMATION: frame"
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LOCATION: 3444.3728
OTHER INFORMATION: /function=
OTHER INFORMATION: frame"
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LOCATION: 7770.8006
OTHER INFORMATION: /fur
OTHER INFORMATION: first
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12218 TCCGCAAGCACCGGCCGCTGTTCGATGACCGGCCGAACACGGTAGCGCTTACCGAGGCCC 12277
                                                                                                  taggeteageaagatetgatgteeteacaetggatgteetggacgtggtgaccaeggace 568
                                                                                                                                                                                              12338 ACCAGGACGACGACGACGACGCCCGTGCAGTCCCTCGGCGACGACGACGCGCCCCG 12395
                                                                                                                                                569 ccccacccgacgtgcacgtgagccgcgttgggggcctggaggaccagctgagtgtgcg 626
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LOCATION: 222..425
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 1109..2014
OTHER INFORMATION: /function- "potential open reading
OTHER INFORMATION: frame"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Beyer Jr., Wayne F.
TITLE OF INVENTION: MYCOBACTERIOPHAGE SPECIFIC FOR THE
TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS COMPLEX
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Richard J. Rodrick, Becton Dickinson and ADDRESSEE: Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/402,066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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atent No. 5612182
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JOMPUTER REDABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1564 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ittle, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 747.1109
OTHER INFORMATION: /fun
OTHER INFORMATION: fram
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LOCATION: 451..747
OTHER INFORMATION: /fur
OTHER INFORMATION: fran
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': 1 Becton Drive
Franklin Lakes
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NAME/KEY: misc_feature
LOCATION: 451..747
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 5382..5747
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 221.425
OCHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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OTHER INFORMATION: frame"
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LOCATION: 1109..2014
OCHER INFORMATION: function- "potential open reading
OTHER INFORMATION: frame"
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NAME/KEY: misc_feature
LOCATION: 2034..2747
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 3444..3728
OCHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 3731.4855
OTHER INFORMATION: /function- "potential open reading
OTHER INFORMATION: frame"
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/402,068
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FUGIT, DONDA R.
REGISTRATION NUMBER: 32,135
REFERENCE/DONCET NUMBER: P-3283
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 3109:.344
OTHER INFORMATION: function-
OTHER INFORMATION: frame"
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OTHER INFORMATION: /function-
OTHER INFORMATION: /groduct- "
                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                      LENGTH: 1564 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 2747..3109
OTHER INFORMATION: /fur
OTHER INFORMATION: fran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 12218 TCCGCAAGCACCGGCCGCTGTTCGATGACCGGCCGAACACGGTAGCGCTTACCGAGGCCC 12277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  509 taggeteageaagatetgatgteeteacaetggatgteetggaegtggtgaeeaeggaee 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12338 ACCAGGACGACCAGGACGACAGCCCCGTGCAGTCCCTCGGCGACGAGCACCGCGCCCG 12395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                449 tececaaggaeetggeeetetteaeteeetatgagatetgggtggaageeaeeaategee 508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34; DB 1; Length 15664;
Pred. No. 3.8;
0; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , NAME/KEY: misc_feature
; LOCATION: 15429..15664
; OTHER INFORMATION: /function= "potential open reading
; OTHER INFORMATION: frame"
US-08-402-066-3
                                                                          NAME/KEY: misc_feature
LOCATION: 11917.12741
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 15154..15426
OTHER INFORMATION: /function- "potential open reading
OTHER INFORMATION: frame"
OTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame"
PATURE:
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LOCATION: 12748.14499
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 14771..15154
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
NAME/KEY: misc_feature
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APPLICANT: Hamilton, Paul T.
APPLICANT: Little, Michael C.
APPLICANT: Little, Michael C.
TITLE OF INVENTION: MYCOBACTERIOPHAGE SPECIFIC FOR THE
TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS COMPLEX
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
ADDRESSEE: Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08402068
Patent No. 5633159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 49.4%;
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1 Becton Drive
CITY: Franklin Lakes
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taggeteageaagatetgatgteeteacactggatgteetggaegtggtgaecaeggaee 568

509

569 ccccacccgacgtgcacgtgagccgcgttgggggcctggaggaccagctgagtgtgcg 626

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12278 recresacecesaceaceacecareansececasesecececesesastreaceece
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LOCATION: 5837..6307
OTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame"
                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: 7770.8006
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                           LOCATION: 6403..7770
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
EATURE:
                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 8033..8236
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 10371.10586
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 11115..11786
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , NAME/KEY: misc_feature
; LOCATION: 15429.,15664
; OTHER INFORMATION: /function= "potential open reading
; OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 9450..1034
OTHER INFORMATION: /function- "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 11917..1274
OCHER INFORMATION: /function- "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 12748..14499
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 15154..15426
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 14771.1515
OTHER INFORMATION: frame" potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 8244..9443
OTHER INFORMATION: /function= "potential open
OTHER INFORMATION: frame"
                                                                                                      misc_feature
6403..7770
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Best Local Similarity
Matches 88; Conserva
                                                                               EATURE:
NAME/KEY:
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367 TTCAGCTCGGCCTGGCGGCGACACACTGCGTCCAGCAGCGGGGGCAGCGCGGCCAGCGCC 308
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                                                   GENERAL ....
APPLICANT: Baxe., Kennet...
APPLICANT: Chien, Kathleen
APPLICANT: Pennica, Diane
APPLICANT: Pennica, Diane
APPLICANT: Wood, William
TITLE OF INCENTION: Cardiac Hypertrophy Factor and Uses;
NUMBER OF SECTENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno. Blvd
CITY: South San Francisco
TATE: California
TSA....
TSA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMBER: US/08/444,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286304
FILING DATE: 05-AUG-1994
                    Sequence 6, Application US/08444083 Patent No. 5571675
                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: patin (Genericch)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 36,70 REFERENCE/DOCKET NUMBER: 8 RELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.18;
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Matches 112; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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IS-08-444-083-6/c
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Gaps

90; Indels

0; Mismatches

Conservative

4.1%; Score 34; DB 1; Length 15664; 49.4%; Pred. No. 3.8;

DD 12218 TCCGCAACCGCCGCTGTTCGATGACCGGCCGAACACGGTAGCGCTTACCGAGGCCC 12277 449 tececaaggacetggecetetteaetecetatgagatetgggtggaageeaetegee 508

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602 gcctggaggaccagctgagtgtgcgctgggtctcaccaccagctctcaaggatttcctct 661
662 tecaagecaagtaccagatecgetacegegtggaggacagegtggactggaaggtggtgg 721
                                        307 GCCGCGTCCAGCCGCAGCCGCTCGTGCACTGGCAGCCCCGCGTGGCTCGGAGCCGGGGCG 248
                                                                                    722 atgaegteageaaceagaeeteetgeegtetegegggeetgaageeeggeaeegtttaet 781
                                                                                                                               247 CTCAGGCCGGCCACCGGCAGCCGCGGCGCGAGAAGCTGGGCAGCCCGAAGGGTTCTCCC 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Pennica, Diane
APPLICANT: Wood, William
AITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1018;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33.4;
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17-may-1995
2011, 435
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
PRIOR APPLICATION DATA:
APPLICATION UNBER: 08/286304
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Genentech, Inc.
STREET: 460 Point San Bruno Bl
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08442745 Patent No. 5624806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION TELEPHONE: 415/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                             Baker, Joffre
Chien, Kenneth
King, Kathleen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Torchia, Timothy REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 46.1
Matches 112; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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MEDIUM TYPE: 5.25 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech
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    662 tecaagecaagtaceagateegetacegegtggaggaeagegtggaetggaaggtggtgg 721
                                                                                                                          247 CTCAGGCCGGCACCGGCAGCCGCGGGGAAAGTGGGGCAGCCCGAAGGGGTCTCCC 188
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                                             307 GCCGCGTCCAGCCGCAGCCGCTCGTGCACTGGCAGCCCCGGGTGGCTCGGAGCCGGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IIILE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor NUMBER OF SEQUENCES: 8
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Pred. No. 2.5;
0; Mismatches 131; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UMBER: US/08/286,304
05-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: Callfornia
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APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08286304
Patent No. 5571893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/2
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                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Baker, Joffre
APPLICANT: Chien, Kenneth
APPLICANT: King, Kathleen
APPLICANT: Pennica, Diane
APPLICANT: Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 25-APR-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 46.1
Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 910/3/1-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1018 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Hasak, Janet E. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
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                                                                                                                                                                                                                     187 TGG 185
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542 atgtcctggacgtggtgaccacggacccccacccgacgtgcacgtgagccgcgttgggg
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662 tccaagccaagtaccagatccgctaccgcggaggacagcgtggactggaaggtggtgg 721
                                                                                                                                                             722 atgaegtcageaaceagaeeteetgeegtetegeggeetgaageeeggeaeegttaet 781
                                                                               307 GCGGGGTCCAGCCGCTCGTGCACTGGCAGCCCCGCGTGGCTCGGAGCCGGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     360 Kb floppy d1sk
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
ATATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/2
FILING DATE: 05-AUG-1994
IOR APPLICATION DATA:
APPLICATION NUMBER: 304
                                                                                                                                                                                                                                                                                                                                                                                                                                            Pennica, Diane
Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUTER READABLE FORM:
EDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATION NUMBER:
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US-08-443-129-6
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Gaps

Score 33.4; DB 1; Length Pred. No. 2.5; 0; Mismatches 131; Indels

Query Match
Best Local Similarity 46.1
Matches 112; Conservative

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367 TTCAGCTCGGCCTGGCGGGGACACTGCGTCCAGCAGCGGGGGGCAGCGGCGGCCAGCGCC 308
                                                                                                                                                                   247 CICAGGCGGCCACCGGCAGCCGCGGGGGGGAAGCTGGGCAGCCCGAAGGGGTCTCCC 188
                                             602 gcctggaggaccagctgagtgtgcgctgggtctcaccaccagctctcaaggatttcctct 661
                                                                                                                                                                                                                               722 atgacgicagcaaccagacciccigccgictcgcgggccigaagcccggcaccgittaci 781
                                                                                                                                       662 tecaagecaagtaceagateegetacegegtggaggaeagegtggaetggaaggtggtgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JABER: US/08/443,952
17-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEE: Genentech, Inc.
1 460 Point San Bruno Blvd
South San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6, Application US/08443952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/233609
FILIND DATE: 25-APR-1994
PRIOR APPLICATION DATA: 08/286304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pennica, Diane
Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  URRENT APPLICATION DATA APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TILE OF INVENTION:
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27845 GCGTGTCCTGCGCGGTGAGCAGCCCTCGGCGTGCAGGGTCCAGTCCGTGGCGCCCTCG 27786 635 caccaccagctctcaaggatttcctcttccaagccaagtaccagatccgctaccgcgtgg 694 සු õ

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755 cgggcctgaagcc 768 | | | | | | 27725 cGcAGCGGACACC 27712

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Search completed: September 28, 1999, 16:40:33 Job time: 7019 sec

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247 CICAGGCCGGCCACCGGCGCGCGGCGAGAAGCTGGGCAGCCGGAAGGGGTCTCCC 188
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                                                                                 Length 1018;
                                                                                 Score 33.4; DB 2; Length 19 Pred. No. 2.5; 0; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application revises...
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Cardiotrophin and Uses Therefor NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04467
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
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APPLICATION NUMBER: 08/2
FILING DATE: 25-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                   4.08;
                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                   Query Match
Best Local Similarity
Matches 112; Conserva'
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; TOPOLOGY: linear
US-08-443-130-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 TGG 185
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                                                                                                                                                                                                                                                              662 tecaagecaagtaccagatecgetacegegagagacagegtggaetggaaggtggtgg 721
                                                                                                                                                                                                                                                                                                      307 GCGGCGTCCAGCCGCAGCCGCTCGTGCACTGGCAGCCCGCGTGGCTCGGAGCCGGGGCG 248
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                                                                                          542 atgtectggaegtggtgaecaeggaeeeeceaeeegaegtgeaegtgageegegttgggg 601
                                               0; Gaps
      DB 2; Length 1018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses TITLE OF INVENTION: Therefor NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
  Score 33.4; DB 2; Length 1 Pred. No. 2.5; 0; Mismatches 131; Indels
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LOASSIFICATION: 435
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STREET: 460 Point San Bruno Blvd
CIIY: South San Francisco
STATE: California
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APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR.1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286304
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08443130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible
    Query Match 4.0%;
Best Local Similarity 46.1%;
Matches 112; Conservative
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Pennica, Diane
Wood, William
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                                                                                                                                                                                                                                                                                                                                                                                                                                           782 tcg 784
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APPLICANT:
APPLICANT:
APPLICANT:
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38; Indels

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Best Local Similarity 59.6%; Pred. No. 8.4;
Matches 56; Conservative 0; Mismatches
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FEATURE:
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US-08-804-227C-7
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                                                                                                                                                   542 atgicciggacgiggigaccacggaccccacccgacgigcacgigagccgcgitgggg 601
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                                                            0; Gaps
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Best Local Similarity 46.1%; Pred. No. 2.5;
Matches 112; Conservative 0; Mismatches 131; Indels
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90 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 MD STORAGE
MEDIUM TYPE: DISKETTE
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TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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FILING DATE: MARCH 7, 1996
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TITLE OF INVENTION: D29
WUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMSTER, ROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA
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STRANDEDNESS: DOUBLE
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RY: U.S.A.
10016
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DB 3; Length 49272

4.0%; Score 33.2;

Query Match

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                                                                  3800 CTTCGCGGTCGGCGTGACCTCGACGCGGTCAAGAACTTCTTCAACGGCTTCTCCGGGCT 3859
                               690 cgiggaggacagcgiggaciggaaggiggiggaigacgicagcaaccagacciccigccg 749
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0; Gaps
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                                                                                                     750 tctcgcgggcctgaagcccggcaccgtttacttc 783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCI(DOS) Text only CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C FILING DATE: February 21, 1997
                                                                                                                                                                                                                                                                                                                                                                                                       2: THOMAS G. PLANT 1501
LILLY CORPORATE CENTER
                                                                                                                                                                                                                          Sequence 7, Application US/08804227C
Patent No. 5876991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
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31329..36071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                            INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
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Best Local Similarity
Matches 93; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46285
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LOCATION:
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NAME/KEY:
LOCATION:
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LOCATION:
FEATURE:
NAME/KEY:
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AAV49280 464 bp mRNA BST 30-DEC-1996 mj45602.rl Soares mouse embryo NDME13.5 14.5 Mus musculus cDNA clone IMAGE:479043 5' similar to SW:ILGB_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W46603 zc32h10.rl
W81301 zd85a12.rl
AA788346 r7c10a1.r
AA255111 mz79d08.r
AIG49345 uc83f01.y
                                                                                                                                                                                                                                                                                                                                                                              R87407 ym88d09.s1
W46604 zc32h10.s1
H14009 EST00035 C
                                                                                                                                                                                         AA049280 mj45d02
                                                                                                                                                                                                                                                                                                                                                                                                                  A1575060 UI-R-G0-N78873 zb17h05.s1
                                                                                                                                                                                                                                                                                                                                                                                                                                          AI074921 0y04d08
AA049278 mj45c04
                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                 Description
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                                                                                                                          SUMMARIES
                                                                                                                                                               a
                        em_est24:*
em_est25:*
em_est26:*
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 em_est22:*
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Match Length
54:
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297.2
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                                                                            3; Search time 2095.87 Seconds (without alignments) 784.921 Million cell updates/sec
                                                                                                                                                   | cccaccttctcatcggctc.....atgggtcgaaaaaggcggga 834
     GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
                                                                                                                                                                                                    2546578 seqs, 986266752 residues
                                                                           September 28, 1999, 15:38:13
                                                  nucleic search, using sw model
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834
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Perfect score:
Sequence:
                                                                                                                                                                            Scoring table:
                                                   OM nucleic
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Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 482)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geissel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan F., Underwood, K., Moore, B.,
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                300
                                                                                                                                                                                                                                                                                                                                                                                           W66776 14-JUN-1996 mRNA mel7blir. Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:387741 5' similar to PIR:B38252 B38252 granulocyte colony-stimulating factor receptor precursor ; mRNA sequence.
                                                                                                                    643
                                                                                                                                       703
                                                                                                                                                                                                               181 CCCTCTTCACTCCCTATGAGATCTGGGTGGAAGCCACCAATCGCCTAGGCTCAGCAAGAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            I 3'], on equal amounts of mRNA from 2 13.5dpc and 2
                                             ctctcaaggatttcctcttccaagccaagtaccagatccgctaccgcgtggaggacagcg
                                                                                                                      acgtgagccgcgttggggggcctggaggaccagctgagtgtgcgctgggtctcaccaccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Apr 14, 1993 this sequence version replaced gi:785250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Marra M/Mouse EST Project
WashU-HMMI Mouse EST Project
WashUnforo University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                               /clone_lib="Soares mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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High quality sequence stop: 359.
Location/Qualiflers
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/db_xref="taxon:10090"
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/clone="IMAGE:387741"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g1375694
W66776.1 GI:1375694
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w66776/c
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DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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COMMENT
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AGACATTCTTACATACCAACTACTCCCTCAAGTACAAGCTGAGGTGGTACGGTCAGGATA 120
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Dec 30, 1996 this sequence version replaced gi:1528951.
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Pred. No. 2.3e-107;
0; Mismatches 2; Indels 0:
                                                                                                                                                                                                                                                                                                                  Washington University School of MedicineP
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="imagE:479043"
/clone_lib="Soares mouse embryo NbMEI3.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
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High quality sequence stop: 437.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                   Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"/strain="C57BL/6J"
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AA049280.1 GI:1755311
EST.
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Best Local Similarity 99.6
Matches 462; Conservative
                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
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                                                              Mus musculus
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JOURNAL
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14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2.]; double-stranded cDNA was ligated becord adaptors (Pharmacla), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Falina Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA866388 428 bp mRNA EST 05-FEB-1999 UI-R-AO-aj-f-04-O-UI-S3 UI-R-AO-B CONVEGICUS CDNA clone UI-R-AO-aj-f-04-O-UI 3' similar to qb|AC003112|AC003112|Human DNA from chromosome 19 specific cosmid R30292, genomic sequence, complete sequence [Homo sapiens], mRNA sequence.
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                                                                                                                                                                       1;
                                                                                                                                              26; Length 482;
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                                                                                                                                           Score 428.2; DB 26;
Pred. No. 4.4e-99;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bonaldo, M.F., Lennon, G. and Soares, M.B Normalization and subtraction: two app.
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                                                                                                                                        Query Match 51.3%;
Best Local Similarity 99.1%;
Matches 441; Conservative
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 428)
Bonaldo, M.F., Lenno
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                                                                                      BASE COUNT
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University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 5242, USA 7m: 319 335 8250
Fax: 319 335 9555
Email: mscares@blue.weeg.uiowa.edu
Oligo-dr track not found, Not I site shown in beginning of sequence 1s likely internal to the message. CDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="pulse (life Technologies)"
/note="Vector: p1713D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1: Site_2: Eco R1; This library consists of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung. Drain, liver, kidney, heart, spleen, ovary, and muscle. The tag is a sting of 3-5 nucleotides present between the Not I site and the oligo-dr track which allows identification of the library of origin of a clone within
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  362 GCGGTCTCGCGGGCTTGAAGCCCGGCACCGTTTACTTCGTCCAAGTTCGTTGTAACCCAT
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Pred. No. 4.7e-89;
0; Mismatches 24; Indels 0;
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/clone="UI-R-AO-aj-f-04-0-UI"
/clone_llb="UI-R-AO"
                                                                                                                                                                                                                                                           /organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                            /strain="Sprague-Dawley
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tf25h01.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2097265 3'similar to SW:IL6B_MOUSE Q00560 INTERLEGKIN-6 RECEPTOR BETA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)
On Apr 7, 1998 this sequence version replaced g1:3034955.
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                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
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NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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./organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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                                                                                'RECURSOR ;, mRNA sequence
                                                                                                                                                                                            AI421423.1 GI:4267354
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1 (bases 1 to 47?)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image:llnl.gov) for further information.
Insert Length: 1552 Std Error: 0.00
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Pred. No. 4.5e-68;
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/db_xref="taxon:9606"
/clone="IMAGE:1742408"
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High quality sequence stop: 467.
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Best Local Similarity 85.8
Matches 339; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A1394468 462 bp mRNA EST 30-MAR-1999
tf79d12.xl NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2105495 3'
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Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases) 10 462)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Ndional Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
On Feb 17, 1998 this sequence version replaced g1:2887603.
                                                        9999ccaccgctgaggggctctactggaccctcaatggtcgccgcctgccctctgagctg 120
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                                                                                                                                                                                                                                                     Library Preparation: M. Bento Soares, Ph.D.,
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/db_xref="taxon:9606"
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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Seq primer: -40UP from Gibco
High quality sequence stop: 454;
Location/Qualifiers
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1. (Dases: 1 to 466)

NCI-GGAP http://www.ncb1.nlm.nih.gov/ncicgap.
NAI-GGAP http://www.ncb1.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)

On Jan 19, 1998 this sequence version replaced gi:2287379.
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Tel: (301) 496-1550
Email: Robert-Strausberg@inh.gov
Email: Robert-Strausberg@inh.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
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Pred. No. 3e-66;
0; Mismatches 53; I
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Best Local Similarity 86.2%;
Matches 330; Conservative
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Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dass 1 to 466)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NATional Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

(Upublished (1997)

On Jan 19, 1998 this sequence version replaced gi:2151491.
                                                                                                                             Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Email: Robert_Strausbergenih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (Info@image.llnl.gov) for further information.
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Chordata; Craniata; Vertebra
Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                             /db_xref='taxon'9606"
/clone='InAcE:1741879"
/clone=lib='Soares_fetal_lung_NbHL19w"
/dev_stage="19 weeks"
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llarity 85:9%; Pred. No. 7.6e
Conservative 0; Mismatches

    .466
    /organism="Homo sapiens"

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Seq primer: -400P from Glbco
High quallity sequence stop: 466.
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                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="839C02; 821G11; 4; 4p15.33-4p16.1; 4p15.33-4p16.1"
/clone="INAGE:1705398"
/clone_lib="Soares_fetal_heart_NbHH19W"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 tgcctctatgttggcttgcccctgagaagcccttaacatcagctgctggtcccggaac 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ggggccaccgctgaggggctctactggaccctcaatggtcgccgcctgccetctgagctg 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323 TGCCTCTATGTTGGCCTGCCCCAGAGAAACCCGTCAACATCAGCTGCTGGTCCAAGAAC 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               466 bp mRNA EST 29-OCT-1998
Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
379 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 35.6%; Score 297.2; DB 43; Length 466; Best Local Similarity 85.9%; Pred. No. 7.6e-66; Matches 329; Conservative 0; Mismatches 54; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                    1 others
   Insert Length: 1599 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 454.
Location/Qualifiers
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                                                                                                                                               /sex="unknown
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IMAGE:1741879 3'
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BASE COUNT ORIGIN

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AI187074
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed
                                                                  Soares_fetal_lung_NbHL19W Homo saptens cDNA clone N6 3' similar to TR:Q16354 Q16354 PROLACTIN RECEPTOR ;;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 431)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Conscrium (info@image.llnl.gov) for further information.
Insert Length: 1615 Std Error: 0.00
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Soares and M.Fatima Bonaldo. This ibrary was construction the same fetus as the fetal heart library. Soares
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 407.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /map="4p16.1-4pter"
/clone="IMAGE:1930606"
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                                                                                                                                                           AI333812.1 GI:4070371
                                                     431 bp
                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
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                                                                                                          mRNA sequence
                                                                       qp93e12.x1
                                                     AI333812
                                                                                                                                          NID
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normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbHH19W." 175 c 128 g 74 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1667 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 CCCACGCTTCTCATCGGCTCCTCCTGCTGGCCACCTCACTGCACGAGCCCACCA 160
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                                                                                                                                                                           AI187074 447 bp mRNA EST 29-OCT-1998 qe38a03.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1741228 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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Pred. No. 2.4e-58;
0; Mismatches 50; Indels 0;
183 ATGAAGGACTTGACCTGCCGCTGGACGCCCAGGGCCCCACGGGGAGACCT 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1741228"
/clone_lib="Soares_fetal_lung_NbHL19w"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This crows (info@image.llnl.gov) rollinger London 1667 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nlh.gov
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Local Similarity 85.6%; Pr
les 297; Conservative 0;
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1 (bases 1 to 447)
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Unpublished (1997)
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reaction. The driver was PCR-amplified cDNNs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-348479."
                                                                                                                                                                                                                                                                                                                                         AI269388 417 bp mRNA EST 27-JAN-1999
q126b05.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1857585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /Organism="Homo saplens"
/db_xref="taxon:9606"
/clone="IMAGE:1897585"
/clone=lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 417)
NCI-GGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
NAtional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergfaih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1634 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop: 406.
Location/Qualiflers
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85.8%;
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Best Local Similarity
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Length 417;

Score 245; DB 44; Pred. No. 1.3e-52;

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AI670108 385 bp mRNA EST 14-MAY-1999 we65503.x1 Soares_thymus_NHFTh Homo sapiens cDNA clone IMAGES.2345981 3' similar to TR:075462 075462 CYTOKINE-LIKE FACTOR-1 AI670108
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 385)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -400P from Gibco____
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Unpublished (1997)
On May 9, 1996 this sequence version replaced gi:1133091.
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/dev_stage="fetal"
/lab_host="DH10B (phage-resistant)"
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/db_xref="taxon:9606"
/map="2"
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High quality sequence stop: 372.
Location/Qualifiers
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Hiller, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry Meg, J.,
Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
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2X56f01.sl Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone
IMAGE:486841 3', mRNA sequence.
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   by Bento Soares and M. Fatima Bonaldo.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                           Score 217.8; DB 50;
Pred. No. 1e-45;
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High quality sequence stop: 388.
Location/Qualifiers
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/db_xref="GDB:376055s"
/db_xref="taxon:9606"
/map="12p"
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Eukaryota; Metazoa; Chordata;
Eutheria; Primates; Catarrhini
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AA042914.1 GI:1522430
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85.3%;
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156 c
                                                                                                                                                                              Best_Local Similarity 85.3
Matches 243; Conservative
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AUTHORS
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double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the No
and Eco RI sites of the modified pT713 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo I others
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                                                                                                             /note-"Organ: uterus; Vector: pT/T3-Pac; Site_1: Not Site_2: Eco RI; 1st strand cDNA was primed with a Not oligo(dT) primer [5'
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 410;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
1 (bases 1 to 312)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
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Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
/clone="IMAGE:486841"
/clone_lib="Soares_pregnant_uterus_NbHPU'
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97044477
On Mar 10, 1998 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                        45;
                                                                                                                                                                                                                                                                                                                                                                                                       Score 200; DB 27;
Pred. No. 3.4e-41;
0; Mismatches 45;
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UI-R-GO-ut-h-08-0-UI.83 UI-R-GO Rattus
UI-R-GO-ut-h-08-0-UI 3', mRNA sequence.
AI579568
                                                                 /dev_stage="adult"
/lab_host="DH10B"
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                                            /sex="female'
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Best Local Similarity 84.7%;
Matches 271; Conservative
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Query Match
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//dev_stage=__dult"
//deb_host="DH10B (Life Technologies)"
//note="Vector: pr7t33-Pac (Pharmacia) with a modified
//note="Vector: pr7t33-Pac (Pharmacia) with a modified
polylinker; Site__1: Not I; Site__1: Soc Ri; The UI-R-GO
library is a normalized library constructed from a
mixture of rat tissues (nodose ganglia, dorsal root
ganglia, and tifgeminal ganglia). The tag is a string of
6 nucleotides present between the Not I site and the
0 ligo-dT track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6:
791-806, 1996."
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Normalization and subtraction: two approaches to facilitate gene
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CDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On May 18, 1998 this sequence version replaced gi:3138307.
Email: msoares@blue.weeg.ulowa.euu
Oligo-dT track not found, Not I site shown in beginning c
Sis likely internal to the message. cDNA Library Preparati
Soares Lab Clone distribution: clones will be available of
Research Genetics (www.resgen.com)
Seq primer: Mi3 Forward.
Localion/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 198.4; DB 48; Length 332;
Pred. No. 7.9e-41;
0; Mismatches 16; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eutherla; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 319)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AIS74687 319 bp mRNA EST
UI-R-GO-uc-b-11-0-UI.s1 UI-R-GO Rattus norvegicus
UI-R-GO-uc-b-11-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                289 CAGCAGTCAGGGGACAATCTGGTGTGTCACGCCCGAGATGGCAG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cagcagtcaggagacaatctggtgtgtcacgcccgagacggcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Soares, MB Program for Rat Gene Discovery and Mapping
                                                                                                                                                           /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xxef="kraxon:10116"
/clone="UI-R-G0-ut-h-08-0-UI"
/clone_lib="UI-R-G0"
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97044477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.8%;
92.9%;
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Matches 208; Conservative
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AI574687.1
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A1574687
LOCUS
DEFINITION
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ORIGIN
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AUTHORS
TITLE
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MEDLINE
COMMENT
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KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
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/urania="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="Laxon:10116"
/db_xref="Laxon:10116"
/map="6p21:3; 5q3"
/clone="U1-R-GO-uc-b-11-0-UI"
/clone="U1-R-GO-uc-b-11-0-UI"
/clone="U1-R-GO-uc-b-11-0-UI"
/dow_stage="adult"
/dow_stage="ad
451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 8250
Email: msoares@blue.weeg.ulowa.edu
Oligo-dr track not found, Not I site shown in beginning of sequence is likely internal to the message. CDNA Library Preparation: M.B. soares Lab Clone distribution: clones will be available through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 TCNCGTCTCCTCAACACCTCCACCCTGGCCTTGGCCTGGCTAACCTTAATGGGTCCAGG 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ggggccaccgctgaggggctctactggaccctcaatggtcgccgcctgccctctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 1 others
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Pred. No. 1.1e-37;
0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 t
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Job time: 3285 sec
                                                                                                                                                                                                                                                                                                                                                                                  Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 CAGCAGTCAGGGGACAATCTGGTGTGTCACG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
g
                                                                                                                                                                                                                                                                                                                                                                                                                                    Seg primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.3%;
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'note="
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                                                                                                                                   correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon. If this cannot be the entire insert of the sequence clone. If may be shorter because we only sequence overlapping sections once, or longer, because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid 9810 lies between 259 and 588 in the Asel-B genomic restriction fragment.

In 33320
prediction is based on positional base preference in codons using a specially developed Hidden Markow Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778 (1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
lun/cgi-/www.nih.go.jp/
lun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="SC9B10.02"
//gene="SC9B10.02, unknown ATP/GTP binding protein, len:
362 aa; similar in N-terminus to other ATP/GTP binding
proteins eg. COBW_PSEDE P29937 cobw protein from
pseudomonas denitrificans (353 aa), fasta scores; opt: 302
z-score: 390.2 E(): 1.4e-14, 30.1% identity in 366 aa
overlap. Contains PS00017 ATP/GTP-binding site motif A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPSADPHSTTGGRSPDSGVDMYTRKNATGRFGSAAAGMLLATAGISLAARRRRREAA
WHERLLELEELAIRROSLAHQORMHWELLTRAIDDPSLAEVIDTYOKSIPARRROF
YANAWYVNLYHVHRAGLLDQEGLGGRLREFFQSPVFREYWEATRNMRAALDQNSDEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MRGADVFQGAGPCDPRFPPCASSPPPRRSAPLGTLEAAAPSIAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KTDRATDAERVLGLVHSLVGGAAVVPATYGRIDPEELYDCREGEERVGQLSFDDLHDH
SEGGAHADHLHAAYDTLSFVSGLPLDPRRLMRFLDSRPKGLYRIKGYVDFGPYDTRNR
YAVHAVGRFLRFYPEPWTPAGAAGGSGAPETGRTQLVLIGSGIDAAALGEELDACRRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'translation="MGQRSTPQQIPVVVLAGFLGSGKTTLLNHLLHRSGGSRIGAVVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGLAEPQELVRMLLASEQPGIVYGGLVEVVDAAEFDDTRARHPEIDRHLALADLVVVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="hypothetical protein SC9B10.01c"
protein_id="CAA15791.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="possible RBS upstream of SC9B10.02"
997. .2085
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protein_id="CAA15792.1"
db_xref="PID:e1202333"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(159. .905)
/gene="SC9B10.01c"
/note="SC9B10.01c, unknown, len: 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Streptomyces coelicolor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(1. .6675)
/note="overlap with Cosmid St5B8"
complement(159. .905)
/gene="SC9B10.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGLVVDALAKDFEDTDTDEWWVVGTPPHD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _xref="SPTREMBL:050508"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'db_xref-"SPTREMBL:050509"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'db_xref="PID:92661687"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'db_xref="PID:92661688"
'db_xref="GI:2661688"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="PID:e1202332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:1902"
/clone="cosmid 9B10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="SC9B10.02"
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/gene="SC9B10.02"
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trans1_table=11
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gene

CDS

RBS

gene

FEATURES

CDS

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fine 1818 as; similarity (strongest in N-terminus, around active site) to DNA gyrase subunit A from many organisms of GYRAMYCTO 00770 dna gyrase subunit a (ec 5.99.1.3) from Mycobacterium tuberculosis (838 aa), fasta scores; opt: 1835 z-score: 1379.9 E(): 0, 42.48 identity in 768 as overlap; and to S. coelicolor GYRA_GYRCO P35885 dna gyrase subunit a (ec 5.99.1.3) (864 aa), fasta scores; opt: 1886 z-score: 1425.4 E(): 0, 42.98 identity in 788 aa overlap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALGTEGGVVKRVVPDY PSNKDELEVITLKDGDRIVGGVELRTGDEDLYFITDDAGLLR
YQASQVRPQGRPAGGVAGVKLADGAKVISFTAVDPAADAVVFTVAGSRGTLDDSYQTT
AKLTPFDQYPRKGRATGGVRCQRFLKGEDCLAFAWAGATPALAAQKNGTPAQLPDTDP
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LTAMEESFGINNVALVDGQPLTLGLKELLEVYLDHRFTVVRRRSEFRRSKRRDRLHLV
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/gene="SC9B10.04"
/fonte="SC9B10.04"
/note="SC9B10.04"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WYDVGSRHEVKGRIGLAHLFEHLMFQGSAQVKGNGHFELVQGAGGSLNGTISF!
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/note="possible RBS upstream of SC9B10.03c"
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product='nDA gyrase-like protein"
'protein_id="CAAI$793.1"
db_xref="FID:e1202334"
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                                                                                             /gene="SC9B10.03c"
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en: 818 ==
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/db_xref="PID:e1202335"
/db_xref="PID:92661690"
/db_xref="GI:2661690"
/gene="SC9B10.03c"
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/transl_table=11
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                                   18469 GCCCGGCTACCACATCTGGTTCATCTTCATGCGGTCGATGATGCTGCTGGACATCAGCAG 18410
                                                                                                        GCACCGCTGGGAGCGGATGGCCCCGATCAACGCGATGGCGTGGGCGATCCAGACCATCGC 18350
                                                                                                                                                                           18349 CAAGCCCTCCCAGTTCGAGG -- TCAAGGAGCCGCTGCCGCGGGGTCGTGGCCCGGGA 18293
                                                                                                                                                                                                                                                    18233
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Eucheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 183800)
Waterston,R.H.
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Submitted (25-APR-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Jun 5, 1999 this sequence version replaced g1:4680445.
* NOTE: This is a 'working traft' sequence. It currently a consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
   gatccgctaccgagtggaggacagtgtggactggaaggtggtggacgatgtgagcaacca
                                                                      gacetectgeogeetggeoggeetgaaaceeggeacegtgtaettegtgeaagtgegetg
                                                                                                                                             18292 GGCCGCCAAGTGGCTGCCGCGCGGGGGCGGCTCGACCGCGGACTTCCTGTCCTACCC
                                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                  13037: contig of 13037 bp in length
13054: gap of unknown length
183800: contig of 170746 bp in length.
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Homo sapiens clone NH0429J10, WORKING DRAFT
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Pred. No. 0.95;
0; Mismatches 136;
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38622 c 35111 g 51289 t
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/db_xref="taxon:9606"
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Submitted (28-NOV-1997) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO ISA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 70H, UK
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Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agaS, agaZ. DNA gyrase-like protein; FAD-dependent oxidoreductase; ferrochelatase; hemH; phosphocarrier protein hpr; ptsH; putative hydroxlase; putative thimidine kinase; subB; tagatose 6-phosphate kinase; tagatose-bisphosphate aldolase; thiosulfate sulfurtransferase; transcriptional regulator; zinc
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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Details of S. coelicolor sequencing at the Sanger Centre are.
Details of S. coelicolor sequencing at the Sanger Centre are.
Wavilable on the World Wide Web.
(URL; http://www.projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Redenbach, M., Kleser, H.M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.

Kast of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
2774 GGCGCCCCTTCCTCCTCCTCCCTCCCGTCCTGGGGCCGGAGGGCGGGGGGCCGGGG 2833
                                                                                                                                                                                                                                                                                               941 agtggcgagdctggatgcagaagtcgcacaagacccgcaaccagcacaggacgaggggat 1000
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                                                                                                                                                                                                                                                                                                                                                       2954 GGCGCCGGGAGCGCCGGGTACAGTCGGGTGGCTCCGCACCTCGAGTTCCGGGCGTCTT
                                                             cgtgcgaaccgcggggggggaggccgagctcggggccggtgcggcgcgagctcaagcagt
                                                                                                                  tectgggetggetcaagaageacgegtaetgetecaaceteageétecgeetetaegaee
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2 (bases i to 33320)
Parkhill, J., Barrell, B.G. and Rajandream, M.A. Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
SC9B10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOURCE
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ö

Gaps

ö

Indels

Length 183800;

3.58;

Best Local Similarity 48.9 Matches 130; Conservative

Query Match

E-value

note="Plam match to entry PF00550 pp-binding, Phosphopantetheine attachment site, score 76.90, 1.2e-19"

note-"PS00455 Putative AMP-binding domain signature.

;232. .5424 /gene="SCE63.01"

misc_feature

misc_feature

gene="SCE63.01"

AMP-binding

misc_feature

note-"Pfam match to entry PF00501 AMP-binding, MP-binding enzyme, score 448.70, E-value 5.2e-131"

'gene="SCE63.01"

```
PF00668 DUF4, Domain of unknown function, a Pfam match to entry PF00668 DUF4, Domain of unknown function, a Pfam match to entry PF00975 Thioesterase, Thioesterase domain and two Pfam matches to entry PF0050 pp-binding.

Phosphopantetheine attachment site. Each PF00501 contains a Prosite match PS00455 Putative AMP-binding domain Phosphopantetheine attachment site.

Phosphopantetheine attachment site.

Phosphopantetheine attachment site.

Codon start—
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RCAGDAPAWQPLPVQYADYALWQQEILGDDTDPDTLAGRQLAYWKQQLAGLPERLDLP
TDRPRPATADHTGDRVEFALPADLHTRLTELARATDTTLIYWVLQAALATLLTRHGAGE
DIPIGTPVAGRTDDATDHLVGFFVNTLVLRTDTSGNPTFRDLLTRYRDTDLTAYTHQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="RLRPAETLTGFLRRLQGEQARLIDHOWVGLAEIQRWAGSGELFD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AERFTDLFEEGVARTPGKTALIAPDGRLFYAELDAAANRLARRLVELGVGPERHVAVA
VGRRTELVVGMLAVLKAGGAYVPVDPEYPPDRIRHMIQDADPALVLTTSDVDDRIGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSSQAPDISGLSVMQASASFDQSVGSLHAPLISGGCVRLTDLRALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGEVYLAGVQLARGYLGRGGLTAERFTADPFGAPGSRMYRTGDVAHWNEAGELVFAGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADROVKLRGYRIELGEIEAAVAGGPGVRQAAVVLREDRPGDQRLVAYVVPDPGHNDEA
AARARLALSLPDFMAPSAFVALDALPLSPNGKLDRAALPAPTYTGRTAGRAPRTPAEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .LCDLYAEVLSLPGVTVDDDFFDLGGHSLLATRLVSRVRTTLGAELSIRQFFEAPTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alavvlagagraraaltarprperlplsyaqorlwflhilegpsptyniptvlrisgp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRPDALRAALLDVVGRHESLRTTFTEDERGÄRQVVHPÄDGVRPVFETAESTEADYEAD
LARAARHAFDLGAEIPVRARLLRLSEREHVLLLLVHHIASDAWSRGPLAQDLTAAYTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPFERLVEALNPTRSLTHHPLFOVVLSLRSTAPRRADGEGAPALPGGLRVSGTGGAAA
TAAKVDLGFSVTERRAADHTFDGVAGVLDFRTDLFDRGTAQGLVDRLVRVLADAAAHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Syaelnaranrlarllvargagperlvalalprsaelpvavlavakagaaylpldpah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APLLPGHPAYVIYTSGTTGRPKGVTVTHSGLPALLDIFTSQLDVVPGSRVLHHLSPAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGGFWELAMGLLTGAALVVVEPGTVPGPALAALAVRHRVTHAAITPAVLQLIPEGALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Pfam match to entry PF00668 DUF4, Domain of unknown function, score 335.30, E-value 6.9e-97"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAMVFENYPLNSSRGRPPGAAPDADLPTVLGVRSKDQMHYPLGLLALPRETLRFSLGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPOVFDPARVEAVIAAFRRALRTVLDAPDTRVGAVALLDPEVRGTVLEKWSGSDDVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NTGTSLGRHSGTALTDADRAAPLLPGHPAYVIYTSGTTGRPKGVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  || CPPELVARWSAGRLMRNSYGPTETTVCATMSAPLAGAAVPP1GRPIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DRRLVGYVVPDAGASVDPGALRQALRGSLPEYMVPAALVVLDALPLTTNGKLDHRALP
APEYRTVEGRSPRTPREEALCRLFAEVLGLELVGLDDGFFDLGGHSLLAIRLVERVRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             elgeelgvrdlfaaptvadlavrlaarggrepmerllplraagtarpvfcvhpgsgms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #SLGGNVAFAMARELRARGOEVELLAFLDAYPRRAGAGPEAPLAEVFAHNLRDAGFDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEEELTGGRFPTARYRAFLNAAGDPMGRLDEAELAAVLEVFMNNAALMRGHTPGTYDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'L'VLAAERADGDKLARRGAESWRPHVRGRIERVGVDADHLGLVQSDAALAVIGRALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAERIAGTLDDAAPVALLTTAAVAAGLPDTDVPRLLLDEEPAAGGGEDAADLTDADRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGDLVRHRADGDLEYLGRTDTQVKLRGMRVEPAEIEAVTAGLPGVAQAAVLVREDTPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVTVVNVYGPTEATGHCLEHWIAPDRTVEPGPVPIGTPHEGVRVXVLDSALRPVAPGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DRPLSRIDVLGPRERHRVVEEWNATAKGLAPATLPELFERHVRERPGAEAVVAGDTSI
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Phosphopantetheine attachment site, score 78.40, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"PS00455 Putative AMP-binding domain signature."
2046. .2238
/gene-"SCE63.01"
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/gene="SCE63.01"
/note="PS00012 Phosphopantetheine attachment site."
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/note="Pfam match to entry PF00501 AMP-binding,
AMP-binding enzyme, score 385.20, E-value 6.6e-112"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRLDPATGHAASAAVPETEGVTAMNPSPEPAPSPESLDSTEVA
                                                                                                                                                                                                                                                                                                                                                                                               /product="CDA peptide synthetase III"
/protein_id="CAB38876.1"
/db_xref="PID:e1393918"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref-"PID:q4490979"
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/gene="SCE63.01"
/note="Pfam match
                                                                                                                                                                                                                                                                                                                             table-11
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                                                                                                                                                                                                                                                                                            /codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .6e-20
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to many eq. TR.052809 (EMBL:AJ22399) from the vancomycin blosynthesis cluster of Amycolatopsis orientalis (276 as) fasta scores; opt: 892, z-score: 1028 9, E(): 0, (50.9% identity in 271 as overlap) and TR.057982 (EMBL:AF003947) Pcal; single polypeptide combining 3-oxoadipate enol-lactone hydrolyzing and 4-carboxymuconolactone decarboxylating activityfrom Rhodococcus opacus (400 as) fasta scores; opt: 28% z-score: 335.4, E(): 2.3e-11, (32.0% identity in 256 as overlap). Contains Pfeam match to entry PF00561 abhydrolase, alpha/beta hydrolase fold, society 27.80, E-value 2.2e-19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18949 Cerceactreacececeacecearererrecrasses careaceces and consecutive and the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18889 CCCCGTCACCCCGCACCGCGCCACGACGACTTCCCCGACGTACCCGGCATGCTCGGCGA 18830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18769 GGAGCIGGAGCAGGCGIICACCGACAICGAGACCGCGIICGGCGACGGCIIGGGAGCGGGC 18710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 egiggecacgecegigacggeageatectggetggetectgectetatgttggeetgee 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 cccagagaaacccgtcaacatcagctgctggtccaagaacatgaaggacttgacctgccg 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ctggacgccaggggcccacggggagaccttcctccacacca---actactccctcaagta 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                  /note="Pfam match to entry PF00975 Thioesterase,
Thioesterase domain, score 139.00, E-value 8.5e-38"
6360. 7178
5301. 5348
/gene="SCE63.01"
/note="PS00012 Phosphopantetheine attachment site.
/4900. 6219
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="SCE29.02, probable hydrolase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 50.6; DB 1;
Pred. No. 0.47;
0; Mismatches 449;
                                                                                                                                                                                                                                                                         /gene-"SCE29.0"
6360. 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
/label=SCE29.02
                                                                                                                    5490. .6219
/gene="SCE63.01"
                                                                                                                                                                                                                                                                                                                                                                                                 'gene="SCE29.0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     score 77.80, E /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                               misc_feature
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IHGGSGRDTLAGGAGADVFRPSELTDSYRTDSASYADLITDFDASEDRIDLSGLGFSG
LGNGYGGTLALQVNSAGTRTYLKSYEANAAGERFELSLDGDLSGLDGESHLVFDERVVL
                                                                                                                                                                                                                                        AGGDGNDTLSGGSAAEELLGGAGNDSLSGGAGNDTLDGGAGRDTLSGGSGSDIFRFGD
ALDSFRNYNSGANVTDSTADFTHGADLIDLSALGYTGLGDGYNGTLAIVLNDAGTKTY
LKDRGGDAEGNRFETALEGNHADQLDASDFIFATAAAATGIEVVGSTPAEEQPVV"
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                                                                     LDGGVGRDTLTGGAGADTFRFSAREDSYRTASTSFTDLTTDFDPAQDRIDLSALGFTG
LGDGYDGTLLVTTGSGGSRTYLKSLEADAEGRRFEIALDGDFVGLLDASNLIFERPAI
BGDAGDNALLGTSVAETLLGHAGNDTLDGAGGDDILVGGAGSDSLTGGAGADVFRFDA
                                                                                                                                              LSDSQRNYDTGDNQGDRITDFAVGEDKLDVSALGFTGLGDGYNGTLVLVLNSAGDRT\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABC transporter; acyl carrier protein; acyl carrier protein synthase; CDA peptide synthatase II; cadaps3; excisionase; hydrolase; integrase; isomerase; myo-inositol phosphate synthase; oxygenase; phosphopantethelne attachment site; phosphotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1037 GAAGGCGTGCTCCAAGATGACCAGCGACATCACCCTGCAGAACGCCGATATCCACGGC 1096
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces

Saunders, D.C. and Harris, D.

Unpublished

AUTHORS

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un codons is given for each of these may be intraced; including the highest social match found by fasta -o is given for Usually the highest social match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markow Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994) and the Frameplot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, qtg, ttg or (att)) which is preceded by an upstream initiation codon. If this cannot be identified we choose the most upstream initiation codon. If this cannot be identified we choose the most upstream initiation codon. If this cannot be identified we choose the most sequence clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlapp with cosmids E63 and E39 on the Asel-E genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="SCE63.01, partial CDS, cdaPS3, CDA peptide synthetase III, len: >332aa; Constitutes the the majority of cdaPS3, CDA peptide synthetase III, part of the calcium-dependent antibiotic (CDA) biosynthetic cluster from Streptomyces coelicolor. CDA is a peptide antibiotic which is synthesised non-ribosomally by a putative multifunctional peptide synthetase enzyme. This partial
                                                                                                                          project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Details of S. coelicolar sequencing at the Sanger Centre are available on the World Wide Web.

(WEL, http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC/B7.01c. SC (S. coelicolor), 787 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 physical map
                                                                                                                 coelicolor sequencing proje
Campus, Hinxton, Cambridge
                                                                                               Submitted (12-MAR-1999) Streptomyces coelicolor sequencing projector tentre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBLO 15A B-mall: barrellesanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk.NR4 70H, UK
                                                                                                                                                                                                                                                                                                                                                        Redenbach, M., Kleser, H.M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical maje for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
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coupling. Contains two Pfam matches to entry PF00501
                                       and Rajandream, M.A.
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2 (bases 1 to 26477)
Bentley,S.D., Parkhill,J., Barrell,B.G.
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/db_xref="taxon:1902"
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RFEVALDGDHTGDLSAANVVFAATGTTTELEVLGDSGTQAGAIV"
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YYGAQDVQILDNQIHDNSQNGAYAEVLLQSYDDIAGVSGNFYYTTGTWLEGNVISGSA
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:DLTLDGNRDNLSARVDGWFNGYIPGQDGADRDVTLERVEIREMSGYGFDPHEQTINL
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DALSGTEAHETLLGQAGDDRLNGDAGNDILDGGAGRDNLTGGAGADTFRFSARTDSYR
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                                                                                                                                                                                                                                                                                                                                                                                             A family of modular type mannuronan C-5-epimerase genes controls alginate structure in Azotobacter vinelandii Mol. Microbiol. 16 (4), 719-731 (1995) 96065700
gene; algE2 gene; algE3 gene; algE4 gene; mannuronan C-5
                                                                                                                                                                                       Ertesvag, H., Doseth, B., Larsen, B., Skjak-Braek, G. and Valla, S. Cloning and expression of an Azotobacter vinelandil mannuronan
                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Azotobacteraceae;
                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 15759)
Siresvag, H., Holdal, H.K., Hals, I.K., Rian, A., Doseth, B. and
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protein_id="AAA87310.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Azotobacter vinelandii"
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                                                                                                                                                                                                                                             C-5-epimerase gene
J. Bacteriol. 176 (10), 2846-2853 (1994)
                                                     Azotobacter vinelandii (strain E) DNA.
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protein_id="AAA87311.1"
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1: .15759
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290. .1951
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                                                                                  Azotobacter vinelandii
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gene="algE1"
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gene="algEl"
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Ertesvag, H.
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NNVAYNNDRHGENITTSTYDEVATNNVAYGNGGAGLTIQRGSEDLAQPTDILIDGGAY
YDNALEGVLFKATNNVTLQNAEIYGNGSSGVRLYGTEDVQILDNQIHDNSQNGTYPEV
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                                                                                                                                                                 GGAGRDDLTGGTGADTFVFAARTDSYRTDAGVFNDLILDFDASEDRIDLSALGFSGFG
DGYNGTLLVQLSSAGTRTYLKSYEEDLEGRRFEVALDGDHTGDLSAANVVFADDGSAA
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TIRDSVAHDNGLDGFVADFQIGGVFENNVSYNNDRHGFNIVTSNNDFVLSNNVAYGNG
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ODGADRNVTIERVEIREMSGYGFDPHEQTINLTIRDSVAHDNGLDGFVADYLVDSVFI
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EGRRFEIALDGNFAGLLGAGNLLFERTAIEGDAGDNALLGTSAAETLLGHAGNDTLDC
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AGNDILDGGAGRDTLSGGSGSDIFRFGGALDSFRNYASGTNGTDSITDFTPGEDLIDI
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DSASYADLITDFDASEDRIDLSGLGFSGLGNGYGGTLALOVNSAGTRTYLKSFETNAA
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QGRRFEIALDGNFVGQFNDGNLLFDAAPVTGTEGNDNLSGTDAGFTLLGYGGNDTLNG
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DTLGGSDAHETLLGLDGNDRLNGGAGNDILDGGAGRDNLTGGAGADLFRVSARTDSY
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'protein_id="AAA87313.1"
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1. (bases 1 to 11832)
Micola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S.,
Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
Kikuchi,Y.
A NOVEL HARMOPOTETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME
Patent: WO 9811225-A 19-MAR-1998;
MICOLA NICOS ANTONY (WA)
Location/Qualifiers
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ocal Similarity 73.5%; Pred. No. 3e-28;
s 291; Conservative 0; Mismatches 37; Indels 68; Gaps
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A70408.1 GI:4774683
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/rpt_family="Alu"

complement(18270. .18438)

/rote="Predatched exon, program: grail2exons_human_1.3,

frame: 0, quality: excellent, score:
100.000--(18438. .18284) DDS similarity to W66776

mel?bl:rl Soares mouse embryo NbME13.5 14.5 kus musculus

cDNA clone 387741 5, similar to PIR:B38252 B3825

granulocyte colony-stimulating factor receptor precursor
(157. .1); 828 identity,--(18438. .18465) DDS similarity to
|AA042280 mj45d02.rl Soares mouse embryo NbME13.5 14.5 kus

musculus cDNA clone 479043 5' similar to SW:IL6B_MOGSE

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clone 365523 5' (428. 496); 97% identity.~~(13756. .13984)
DDS similarity to AA009693 ze82h02.si Soares fetal heart
NDHH19W Home sapiens CDNA clone 365523 3' (227. .1); 98%
identity.~~(13756. .13984) DDS similarity to AA450010
zx33f04.s1 Soares total fetus ND2HF8 9w Homo sapiens CDNA
clone 788287 3' (228. .1); 99% identity.~"
//rpt_family-mAlu"
14672)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pregnant uterus NDHPU Homo sapiens cDNA clone 490004 3' (1899. 343); 99% identity. -DDS similarity to AA127694 (1899. 343); 99% identity. -DDS similarity to AA127694 clone 490004 5' (77. 125); 90% identity. -(18735. 15713) DDS similarity to W46603 zc32h10.rl Soares senescent fibroblasts NDHSF Homo sapiens cDNA clone 324067 5' (1871. 329); 100% identity. -(18735. 132467 5' (1871. 329); 100% identity. -(18735. 15713) DDS similarity to W46604 zc32h10.sl Soares senescent fibroblasts NDHSF Homo sapiens cDNA clone 324067 3' (299. 321); 100%
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                                                                                                                                                                                                                                                                                                                                                                            15109 CAGCAGGAGCTGGGGTGGCCCTGAGGCTCCAACGGCCATAACAGCTCTGACTCCCCACGTG 15050
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                                                                                                                        1091 aggoogaacccaaactggggccacctctgtaccctcacttcagggcacctgagc--ccct
                                                                                                                                                                                                      cagoaggagotggggccctgagotccaacggccataacagctctgactccacgtg
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Pred. No. 1.4e-55;
0; Mismatches 0;
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Pred. No. 1.5e-39;
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Sequence 16 from Patent W09811225.
A70386
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86.8%;
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Lamerdin, J. E., McCready, P. M., Adamson, A. W., Burkhart-Schultz, K., Gordon, L., Christensen, M., Kyle, A., Ramirez, M., Stilwagen, S., Garnes, J., Danganan, L., Bruce, R., Quan, G., Montgomery, M., Ow, D., Kobayashi, A., Olsen, A.O. and Carrano, A.V.
Sequence analysis of an ~1 Mb region containing the MEF2B gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                frame: 1, quality: good, score: 71.000"

complement(1383. .1444)

frame: 1, quality: good, score: 62.000"

2257. .8516
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Submitted (21-NOV-1997) Human Genome Center, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
Location/Qualifiers
568 ttcctctttcaagccaaataccagatccgctaccgagtggaggacagtgtggactggaag 627
                                                                                                                    Chordata; Craniata; Vertebrata; Mammalia;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                        21-NOV-1997
                                                                                                                                                                                                                                                                                   AC003112 40668 bp DNA PRI 21-NOV-1997
Human DNA from chromosome 19 specific cosmid R30292, genomic
sequence, complete sequence.
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//cell_line="5HL2-B"
//clone_lib="LL19NC03 R chromosome 19 cosmid library
                                  gtcggggggcctggaggaccagctgagcgtgcgctgggtgtcgccacccgccctcaaggat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /standard_name="endogenous retroviral sequence"
/note="HERV9 retroviral sequence"
complement(3269. 3544)
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/db_xref="taxon:9606"
/clone="R30292"
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Eutheria; Primates; Catarrhin:
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complement(571.
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8951. .9254
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AC003112.1 GI:2636669
                                                                                                                                                                   628 gtggtggacgatgtgagcaa 647
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isc_feature complement(928..9555)

isc_feature complement(928..9550)

frome 1, quality; good score; 63.000*

frome: 1, quality; good score; 63.000*

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A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME Patent: WO 9811225-A 19-MAR-1998; NICOLA NICOS ANTONY (AU)
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11	source 1. 1629 /organism="unidentified" /db_xref="taxon:32644" ORIGIN ORIGIN Ouery Match Best Local Similarity 87.8%; Score 799.4; DB 5; Length 1629; Best Local Similarity 87.8%; Pred. No. 2e-146; Matches 872; Conservative 0; Mismatches 121; Indels 0; Gaps 0; Oy 1 accotcaacgggcgccgccccctgagctcccctgtactcaacgcctccaccttg 60 illilli

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OLA NICOS ANTONY (AU)

Location/Qualifiers

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                                                                                               similar to the sequence presented in GenBank Accession Number AC003112*
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119. .1387
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230. .1384
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11arity 100.0%; Pred. No. 2.1e-261;
Conservative 0; Mismatches 0;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1716)
Elson,G.C.A., Graber,P., Losberger,P., Herren,S., Gretener,D., Menod,L.N., Wells,T.N.C., Kosco-Vilbois,M.H. and Gauchat,J.F. CLF-1, a Novel Soluble Protein Shares Homology With Members of the Cytokine Type-I. Receptor Family

J. Immunol. (1998) In press
Elson,G.C.A., Graber,P., Losberger,P., Herren,S., Gretener,D., Menod,L.N., Wells,T.N.C., Kosco-Vilbois,M.H. and Gauchat,J.F. Direct Submission

Submitted (14-APR-1998) Dept. of Immunology, Serono Pharmaceutical Research Institute, 14, Chemin des Aulx, Plan-les-Ouates, GE 1228, Switzerland 1. .1716 /organism="Homo sapiens' A70384 Sequence 14 A70382 Sequence 22 A70388 Sequence 18 A7038 Sequence 18 AC03312 Human DNA AC03112 Human DNA A7038 Sequence 28 A70408 Sequence 28 A70408 Sequence 38 L39996 Azotobacter

AL035707 Streptomy AC007391 Homo sapi

Scoring table:

Database :

Searched:

Title: Perfect score:

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Sequence:

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Human mRNA

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Result No.

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A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME PATENT: WO 98112525.4 19-MAR-1998; NICOLA NICOS ANTONY (40)
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/note-"unnamed protein product"</pre>
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ö cgtgcacgtgagccgcgtcgggggcctggaggaccagctgagcgtgcgctgggtgtcgcc 551 Gaps ö 3.4%; Score 47.8; DB 1; Length 33320; Similarity 43.9%; Pred. No. 1.6; Conservative 0; Missective Query Match Best Local Simi Matches 205;

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671 cagigigaciggaaggiggiggacgatgigagcaaccagacciccigccgccgg 612

732 ctccaagaaagccgggatctggagtgagtggagccaccacagcgctccactccccg 791

15009 crestreseccessiarcaccassacassacascaresecaresesacaresecs 852

15069 GGCCGGGACGACGTCCTGGTCATCGCCTCCGAGCGGAGCCCAAGGAGTCGGCGATGGT 15128

Search completed: September 28, 1999, 16:40:47 Job time: 7034 sec

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                                                                                                                                                                CCCCCACCGACGTGCACGTGAGCCGCGTTGGGGGCCTGGAGGACCAGCTGAGTGTGCGC 627
                                                                                                            900
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                                                                                                                                                                                                                                                CGTCTCGCGGGCCTGAAGCCCGGCACCGTTTACTTCGTCCAAGTGCGTTGTAACCCATTC 807
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  ctgggctctgcccgctccgatgtactcacgctggatatcctggatgtggtgaccacggac
                                                      cccccgccgacgtgcacgtgagccgcgtcggggggcctggagggccagctgagcgtgcgc
                                                                                                           tgggtgtcgccacccgccctcaaggatttcctctttcaagccaaataccagatccgctac
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Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
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Pred. No. 1e-108;
0; Mismatches 2;
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(AMRA-) AMRAD OPERATIONS PTY LTD.
(DZIE/) DZIEGLEWSKA H E.
                                                                                                                                                                                                                                                                                           808 GGGATCTATGGGTCGAAAAGGCGGG
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99.6%;
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Best Local Similarity 99.6
Matches 558, Conservative
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11-SEP-1996; AU-0022
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WPI; 98-260970/23
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WO9811225-A2.
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e.g. meuronal cells

Claim 6; Page 90-92; 182pp; English.

The heamopoletin receptor (HR) NR6.3 is a form of the novel HR NR6.

Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.

Sequence 938 BP; 243 A; 245 C; 272 G; 178 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-5EP-1998 (first entry)
Novel haemopoietin receptor NK6.3 gene.
Haemopoietin receptor; cell proliferation; cell differentiation; cancer, cell survival; therapeutic; neuronal proliferation; drug screening; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                         627
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New isolated haemopoietin receptor - used for developing products
for modulating proliferation, differentiation and survival of cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aagaacatgaaggacttgacctgccgctggacgccagggggcccacgggggagaccttcctc
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/product= "Haemopoietin receptor NR6.3"
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11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS PTY LTD.
(DZIEZ) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Kojima I, Maeda M, Nash A, Nicola NA, Rakar S, Willson
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WPI; 98-260970/23.
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WO9811225-A2
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V27143;
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P-PSDB;
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  Length 1629;
Conservative
Query Match
Best Local Similarity
Matches 872; Conserv
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The Francian modulating products for modulating products for modulating proliferation, differentiation and survival of cells, per modulating proliferation, differentiation and survival of cells, per e.g. neuronal cells fast per sequence was generated by a SN RACE of brain CDNA using CC The nucleotide sequence was generated by a SN RACE of brain CDNA using CC The nucleotide sequence was generated by a SN RACE of brain CDNA using CC Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival HR and a ligand facilitates proliferation, differentiation and survival maintenance or regeneration in an array of configuration configuration, differentiation and survival in vivo. They can be present in the products used for modulating neuronal proliferation, differentiation cc and survival. The products can also be used for detection and diagnosis, sequence 834 BP; 167 A; 274 C; 225 G; 168 T;
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                                          29-SEP-1998 (first entry)
Nucleotide sequence of products generated by 5N race of brain cDNA.
Haemopoletin receptor; cell proliferation; cell differentiation; cancer
cell survival; therapeutic; neuronal proliferation; drug screening; ss;
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                                                                                                                                                                                                                                                       /*tag= a
/product= "Haemopoietin receptor"
                                                                                                                                                                                                    Location/Qualifiers
1..834
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                         (AMRA-) AMRAD OPERATIONS PTY LTD (DZIE/) DZIEGLEWSKA H E.
standard; cDNA; 834
                                                                                                                                                                                                                                                                                                                                                                                    AU-002246.
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11-SEP-1996; AU-002
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The isolated haemopoletin receptor - used for developing products of modulating proliferation, differentiation and survival of cells, e.g. meuronal cells, e.g. meuronal cells.

Example 8; Page 99-100; 182pp; English.

Example 8; Page 99-100; 192pp; English.

Example 8; Page 99-100; 182pp; English.

Example 8; Page 99-100; 
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29-SEP-1998 (first entry)
Unspliced murine NR6 nucleotide sequence.
Haemopoietin receptor; cell proliferation; cell differentiation; cancell survival; therapeutic; neuronal proliferation; drug screening;
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                                                                                                                                                                                                                               11.SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS PTY LTD.
(DZIE-) DZIEDWSKA H A
ALEXANGE W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 87.6
Matches 874; Conservative
                                                                                                                                                                                                          11-SEP-1997; G02479,
11-SEP-1996; AU-0022
                                                                                                                                                                                                                                                                                                                                                            Zhang J;
zar: 98-260970/23
                                                                                                                                                          WO9811225-A2
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New Msolated haemopoietin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells, e.g. neuronal cells, leading the property of the property of the novel HR NR6. The haemopoietin receptor (HR) NR6.1 is a form of the novel HR NR6. Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening. Sequence 1629 BP; 336 A; 541 C; 453 G; 299 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            v27140;
29-SEP-1998 (first entry)
Novel hemopoietin receptor NR6.1 gene.
Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
cell survival; therapeutic; neuronal proliferation; drug screening; ss;
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/product= "Haemopoietin receptor NR6.1"
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(DZIEZ) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
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113: .1355
/*tag= a
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11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
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P-PSDB; W55011.
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New nucleic acid encoding U4 haematopoietin receptor superfamily chain - potentially useful, e.g. for modulating call proliferation or immune response, for treating cancer and auto:immune disease Claim 1; pages 25-26; 38pp; English.
This is the nucleotide sequence encoding the murine U4 protein from the haematopoietin receptor superfamily, used in the method of the invention for the modulation of call proliferation, or the immune response. Transformed mammalian calls are used to produce recombinant U4 protein. The U4 protein is used to screen for specific binding agents, raise antibodies. It is also used as reagents for assays and as tissue markers for isolation of cognate ligands and receptors, and in pharmaceutical compositions which may modulate cell proliferation, cell differentiation, and the immune system (e.g. for treating immune cell differentiation).
                                 1141
                                                                                                                                             aagtegcacaagaccegcaaccagcacaggacgagggatectgeectegggagaeggg 1020
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26-OCT-1998 (first entry)
Nucleotide sequence of the murine U4 gene.
Murine; U4 protein; haematopoietin receptor superfamily;
cell proliferation; immune response; antibody; cell differentiation; autoimmune disease; cancer; allergy; ds.
                60.0%; Score 835; DB 1; Length 16
87.7%; Pred. No. 4.6e-167;
.ive 0; Mismatches 125; Indels
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(GEMY ) GENETICS INST INC.
Collins M, Donaldson DD, Neben T, Whitters M;
WPI; 98-414109/35.
P-PSDB; W59804.
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122. .1399
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Best Local Similarity 87.7
Matches 925; Conservative
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                     1081 ggagacgcagaggccgaacccaaactggggccacctctgtaccctcacttcagggcacct
                                               29-SEP-1998 (first entry)
Novel haemopoletin receptor NR6.2 gene.
Haemopoletin receptor; cell proliferation; cell differentiation; cell survival; therapeutic; neuronal proliferation; drug screenin Mouse.
                                          tgggtgtcgccacccgccctcaaggatttcctctttcaagccaaataccagatccgctac
 ctgggctctgcccgctccgatgtactcacgctggatatcctggatgtggtgaccacggac
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/product= "Haemopoiet
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19-MAR-1998.
11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS PT
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New isolated haemopoletin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells, e.g. neuronal cells, and included cells, 182pp; English.

The haemopoletin receptor (HR) NR6.2 is a form of the novel HR NR6. Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's darivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for differentiation and survival. The products can also be used for differentiation and survival. The products can also be used for drug screening. Sequence 1673 BP; 544 A; 550 C; 474 G; 505 T;
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L, Farley A, Hilton DJ, Kikuchi Y,
Nash A, Nicola NA, Rakar S, Willson
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.1e-167;
les 124;
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Pred. No. 2.1e-
0; Mismatches
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Best Local Similarity 87.8%;
Matches 926; Conservative (
                                                 WPI; 98-260970/23.
P-PSDB; W55012.
New isolated haemopoletin
                                   Zhang J;
WPI; 98-260970/23
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Location/Qualifiers 159. .1436 /*tag= a /product= Zcytor5

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17-MAR-1999 (first entry)

CDNA encoding rat Zcytor5.

Zcytor5; cytokinin-like receptor; down-regulation; growth factor;
maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
cardiac pathology; heart enlargement; Zcytor5 ligand; ss.

Rattus sp.
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01-MAY-1998;
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Disclosure; Page 72-75; 55pp; English.

Disclosure; Page 72-75; 55pp; English.

The present sequence encodes a protein designated Zcytor5, which is caytokinin-like receptor. Soluble Zcytor5 may be administered to caynor-regulate the effects of a growth and/or maintenance factor in thyrold, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-l on cardiac pathologies, so preventing heart on cardiac pathologies, so preventing heart candiagement. Zcytor5 could be used to detect cardiotrophin-l in the blood, and to discover other possible Zcytor5 ligands. A probe on chromosome 19. Antibodies and the and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the candidity Zcytor5 ilgand effects.

The presence of the zcytor5 proper or thromosome 19. Antibodies and the cardiac antibody could be used to purify Zcytor5 and sequence 1724 BP; 350 A; 550 C; 500 G; 324 T;
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down-regulating Zcytor5 natural ligands or detecting cardiotrophin-1
in blood
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13-FEB-1998; US-074721.
01-MAY-1997; US-85030.
01-MAY-1999; US-045287.
01-MAY-1999; US-03890.
(ZYMO ) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner Control S, Presnell SR, Whitmore TE;
P-PSDB; W70862.
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RESULT 5 V70896 ID V70896 standard; CDNA; 1724 BP.

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recombinant
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                                                                                               Human; U4 protein; haematopoietin receptor superfamily; cell proliferation; immune response; antibody; cell differentiation; autoimmune disease; cancer; allergy; ds.
                                                                                                                                                                                                                                                                                                                            15-JAN-1998; U00334.
16-JAN-1998; U00334.
16-JAN-1999; U00334.
16-JAN-1999; U00334.
16-JAN-1999; U00334.
16-JAN-1999; U00334.
16-JAN-1998; U00334.

Collins M, Donaldson DD, Neben T, Whitters M;
WPI; 98-1414109/35.

New nucleic acid encoding U4 haematopoietin receptor superfamily chain - potentially useful, e.g. for modulating call proliferation car immune response, for treating cancer and auto:immune disease claim 1; Page 28; 38pp; English.
This is the nucleotide sequence encoding the human U4 protein from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cacgcccgtgacggcagcatcctggctggctgcctctatgttggcctgccccagag
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llarity 99.2%; Pred. No. 8.3e-276;
Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                    protein"
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1. .1228
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V41689 standard, CDNA; 1579 BP. C40689; 26-007-1998 (first entry) Nucleotide sequence of the human
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Best Local Similarity
Matches 1382; Conserv
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Db 1693 AAAAAAAAAA 1705	RESULT 3 V70894 ID V70894 ID V70894; AC V70894; DT 17-MAR-1999 (first entry). DE CDNA encoding human 2cytor5. KW 2cytor5; cytckinin-like receptor; down-regulation; growth factor; KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1; KW cardiac pathology; heart enlargement; 2cytor5 ligand; ss. FM Key Location/Qualifiers		PT New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g. pr down-regulating Zcytor5 natural ligands or detecting cardiotrophin-1 pr in blood PS Disclosure; Page 63-66; 55pp; English. CC The present sequence encodes a protein designated Zcytor5, which is CC a cytokinin-like receptor. Soluble Zcytor5 may be administered to CC down-regulate the effects of a growth and/or maintenance factor in CC thyroid, heart, and skeletal mascle for example to lessen the effect of conflictorphin-like match or maintenance factor in CC conflictorphin-like match or maintenance factor in CC conflictorphin-like match or maintenance factor in CC conflictorphin-like match or maintenance factor in conflictorphin-like match or example to lessen the effect	enlargement. Zeytors could be blood, and to discover other comprising Zeytors DNA or RNI and integrity of the Zeytors anti-idiotypic antibody could therapeutically to modify Zey Sequence 1690 BP; 319 A.	Similarity 99.3%; Pred. No. 3.9e-276; Length 3; Conservative 0; Mismatches 3; Indels ctcaacggggggggggcctctccggtgtactcaacgcctcctll	
	, 361 , 673 , 421 , 733 , 793	Oy 541 tgggtgtcgccacccgcctcaaggatttcctctttcaagccaaataccagatccgctac 600 [11]	tccactccccgcagtgagcgccgggccgggcggggggggg	acgogtactgctccaacctcagcttccgcctctacgaccagtggcgagcct.	33 GCACGGCGAGGGTCCTGCCCAGATAGCTGTAGGGGGCTCAGGCCACCCTCCT (81 99agacgcagagccgaacccaaactggggccacctctgtaccctcacctcacctcacctcaggacgcagagccgaacccaactggggccacctctgtaccctcacctcacctcacctcacctcaccacgagccgaacgaggacgaggggtggcccctgagcacctcaacggccataacattaggagcccctgagctccaacggccataacataggagcccctgagcccctagagccataacataggagcccctgagcccctaacgaccataacataggagcccctgagcccctaacgaccataacataggagcccctagagcccctcaccccacacggccataacataggagcccctagagcccctagagcccctagagcccctaacgaccataacataggagccaccccacacgagcccctagagcccctaacgaccataacataggagcccctagagcccccaacgaccataacataggagccccccaacgaccataacataggagccccccaacgaccccaacagaccataacatagagagccccccaacgaccataacatagagagccccccaacgaccccaacagaccataacatagagagccccccaacacacatagagagcccccaacacacac	Oy 1199 ctcccacgtgaggccacctttgggtgcacccagtgggtgtgtgt

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isclosure; Page 63-66; 55pp; English.

The present sequence encodes a protein designated Zcytor5, which is the present sequence encodes a protein designated Zcytor5, which is sequence encodes a protein designated to adversely the receptor. Soluble Zcytor5 maintenance factor in syroid, heart, and skeletal muscle for example to lessen the effect for andiotrophin-1 on cardiac pathologies, so preventing heart largement. Zcytor5 could be used to detect cardiotrophin-1 in the lood, and to discover other possible Zcytor5 ligands. A probe and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the integrity of the Zcytor5 gene on chromosome 19. Antibodies and the raleidotypic antibody could be used to purify zcytor5 and arrapeutically to modify Zcytor5 ligand effects.

Solution 274 T;
                                                                                                                                                               NR-1999 (first entry)
encoding human Zcytor5.

Nr5; cytokinin-like receptor; down-regulation; growth factor;
enance factor; thyroid; heart; skeletal muscle; cardiotrophin-l;
ac pathology; heart enlargement; Zcytor5 ligand; ss.
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RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM, Presnell SR, Whitmore TE;
99-034662/03.
B; W70860.
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                                                                                                                                     standard; cDNA; 1690 BP
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in blood

Disclosure: Page 68-70; 55pp; English.

The present sequence encodes an allelic varaint of protein designated

The present sequence encodes an allelic varaint of protein designated

CC Zoytor5, which is a cytokinin-like receptor. Soluble Zoytor5 may be

CC Zoytor5, which is a cytokinin-like receptor. Soluble Zoytor5 may be

CC dactor in thyroid, heart, and skeletal muscle for example to lessen the

CC dactor in thyroid, heart, and skeletal muscle for example to lessen the

CC dactor of cardiotrophin-1 on cardiac pathologies, so preventing heart

CC blood, and to discover other possible Zoytor5 ligands. A probe

CC comprising Zoytor5 DNA or RNA can be used to determine the presence

CC and integrity of the Zoytor5 gene on chromosome 19. Antibodies and the

CC anti-idiotypic antibody could be used to purify Zoytor5 and

thiotypic antibody could be used to purify Zoytor5 and

the complexity of the Zoytor5 gene of promity Zoytor5 and

CC anti-idiotypic antibody could be used to purify Zoytor5 and

therapeutically to modify Zoytor5 ligand effects.

So sequence 1813 BP; 415 A; 604 C; 519 G; 275 T;
                                                V70895 standard; cDNA; 1813 br., V70895; UFLS tentry) V70895; V70895; V70895; V70895; V70895; V70895; V70895; V70896; 
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TE;
                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
88. .1365
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13-FEB-1998; US-074721.

01-MAY-1997; US-045287.

01-MAY-1997; US-850030.

13-FEB-1998; US-023890.

(ZMO) ZMOGENETICS INC.

Adams RL, Foster DC, Gilbert T, Lok S, Presnell SR, Whitmore TE
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Matches 1390; Conservative
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P-PSDB; W70861.
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Human granulocyte Comamonas sp. N-Ac

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on:

September 28, 1999, 16:45:58; search time 303.81 Seconds (without alignments): 1145.509 Million cell updates/sec

US-09-037-657-24 1391 Title: Perfect score: Sequence:

1 accetcaaegggegeegeet......geaaaaaaaaaaaaaaa 1391

IDENTITY_NUC Scoring table:

Searched:

311585 seqs, 125096042 residues N_Geneseq_36:* Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	ore		7.	•	•	•	•	4.,	•	•	•	•	•	•	•	•	•	•	•	٠		•	•	•	•	•	•	•	•	٠	•	•		•										
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Length 1391; Indels

Ouery Match
100.0%; Score 1391; DB 1;
Best Local Similarity 100.0%; Pred. No. 7e-284;
Matches 1391; Conservative 0; Mismatches 0;

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents an expressed sequence tag (EST) used to identify cDNA encoding a protein designated Zoytor5, which is a cytokinin-like receptor. Soluble Zoytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart of cardiotrophin-1 on cardiac pathologies, so preventing heart blood, and to discover other possible Zoytor5 ligands. A probe and integrity of the Zoytor5 gene on chromosome 19. Antibodies and therapeutically to modify Zoytor5 ligand offects, and therapeutically to modify Zoytor5 ligand offects.

Sequence 259 BP; 53 A; 64 C; 81 G; 46 T;
                                                                 741
                                                                                                                       Gaps
                                                                                                                801
                                                                                                                                                               861
                                                                                                                                                                                                        cggcgcgagctcaagcagttcctgggctggctcaagaagcacgcgtactgctccaacctc 921
                                                                                                                                                                                                                  agetteegeetetaegaecagtggegageetggatgeagaagtegeacaagaeeegeaae 981
                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                          cardiotrophin-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g. down-regulating Zcytor5 natural ligands or detecting cardiotrophin-l in blood Example 1; Page 77; 55pp; English.
                                                          ggcaccgtgtacttcgtgcaagtgcgctgcaacccctttggcatctatggctccaagaaa
                                                                                1 GGCACCGTTTACTTCGTCCAAGTGCGTTGTAACCCATTCGGGATCTATGGGTCGAAAAG
                                                                                                         gccgggatctggagtgagtggagccaccacagccgcctccactcccgcagtgagcgc
                                                                                                                                                         ccadaccadadcadacadcadacadacadcadadadacadadaccadadaccadata
                                                                                                                                                                                                                                                                                                                                                                                                                       Expressed sequence tag used to identify human 2cytor5.
Zcytor5; cytokinin-like receptor; down-regulation; growth factor; maintenance factor; thyroid; heart; skeletal muscle; cardiotrophi cardiac pathology; heart enlargement; Zcytor5 ligand; EST; ss. Unidentified.
                                         ö
                  Length 938;
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ZYMO) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
Lok S, Presnell SR, Whitmore TE;
                 DB 1;
            Score 249.8; DB 1
Pred. No. 3.6e-44;
0; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                       V70897 standard; cDNA; 259 BP
          Query Match
Best Local Similarity 86.8%;
Matches 275; Conservative
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                                                                                                                                                                                                                                                                                                                             CAGGTAGGAAAGTTGGG 317
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01-MAY-1998; U08865,
13-FEB-1998; US-074721,
01-MAY-1997; US-045287,
01-MAY-1997; US-850030,
13-FEB-1998; US-023890.
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Length 259;

Score 223.6; DB 1, Pred. No. 9.1e-39;

16.1%; 92.2%;

Query Match Best Local Similarity

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Claim 9; F1g 3; 182pp; English.
The NR6 protein is a novel Haemopoletin receptor (HR). Interaction
between the novel HR and a ligand facilitates proliferation,
differentiation and survival of a wide variety of cells. The HR and it's
derivatives can be used for modulating the activity of the receptors e.g.
to regulate development, maintenance or regeneration in an array of
different cells and tissues in vitro and in vivo. They can be present in
therapeutics used for modulating neuronal proliferation, differentiation
and survival. The products can also be used for detection and diagnosis,
e.g. for cancers or predisposition to cancers, or for drug screening.
Sequence 11832 BP; 2447 A; 3367 C; 3298 G; 2720 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-5EP-1998 (first entry)
Nucleotide sequence for murine NR6 containing additional SN sequence.
Haemopoletin receptor; cell proliferation; cell differentiation; cancer cell survival; therapeutic; neuronal proliferation; drug screening; ss;
                                                                                                                                                                    61 GGAAGGIGGIGGANGAIGIGAGCAACCAGACCIICIGCCG-CIGGNCGGCCIGAAACCCG 119
                                         aggatttcctcttcaagccaaataccagatccgctaccgagtggaggacagtgtggact 622
                                                                                                                                        682
                                                                                                                                                                                                                                        ocgggatctggagtggagtggagccaccacagccgcctccactcccgcagtgagcgcc 802
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New isolated haemopoletin receptor - used for developing products
for modulating proliferation, differentiation and survival of cells,
                                                                                                                                                                                                                    gcaccgtgtacttcgtgcaagtgcgctgcaacccctttggcatctatggctccaagaaag
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         Indels
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(DZIE/) DZIEGLEWSKA H E.
Alexander W. Fabri L., Farley A, Hilton DJ, Kikuchi Y,
Kojima T., Maeda M. Nash A, Nicola NA, Rakar S, Willson
      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 190.8; DB 1;
Pred. No. 1.4e-31;
0; Mismatches 37;
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  0; Mismatches
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Conservative
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Best Local Similarity 73.5
Matches 291; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          803 cgggcccgggcgggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-MAR-1998.
11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
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29-SEP-1998
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The NRG gene encodes a novel Heamopoletin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's products can be used for modulating the activity of the receptors e.g. to requiret development, maintenance or regeneration in an array of aliferent cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening. Sequence 6663 BP; 1462 A; 1852 C; 1715 G; 1634 T;
                                                                                                                   8784 cecccreaccececececececarreracrecrecereacerecaesississacs 8843
                                                                                                                                                                                                          8904 AAGTGCGTTGTAACCCATTCGGGATCTATGGGTCGAAAAGGCGGGAATCTGGAGCGAGT 8963
                                                                                                   tgagcaaccagacctcctgccgcctggccggcctgaaacccggcaccgtgtacttcgtgc 700
                                                                                                                                                                          --aggtggtggacgatg
                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequence of Murine NR6.
Haemopoietin receptor; cell proliferation; cell differentiation;
cancer; cell survival; therapeutic; neuronal proliferation; drug;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 190.8; DB 1; Length 6663;
Pred. No. 1.2e-31;
0; Mismatches 37; Indels 68:
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(AMRA-) AMRAD OPERATIONS PTY LTD.
(D2IE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "No start or stop codon given"
                                                                                                                                                                                                                                                                ggagccaccccacagccgcctccactccccgcagtg 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product- "Murine NR6"
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1182. .1744
/*tag= a
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Best Local Similarity 73.5%;
Matches 291; Conservative (
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3434 GIGACCACGGACCCCCACCCGACGIGCACGIGAGCCGCGIIGGGGGCCIGGAGGACCAG 3493

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469 gigaccacggaccccccgacgigacgigacgigagccgcggggggcciggaggaccag 528

Gaps

68;

529 ctgagogtgogctgggtgtcgccacccgcctcaaggatttcctctttcaagccaaatac 588

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3554 CAGAICCGCIACCGCGIGGAGGACAGCGIGGACIGGAAGGIGCCCGTCCCGCCCCGGACC 3613
                                                                                        ggagccaccccacagccgcctccactccccgcagtg 796
cagatccgctaccgagtggaggacagtgtggactgga-
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September 28, 1999, 16:40:33 ; Search time 152.56 Seconds (without alignments) 835.882 Million cell updates/sec
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/cgn2_6/ptodata/2/ina/5D_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS9_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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		7 Application C 879892 ORMATION:	Coulle, Pl Smet, C Lucas, Sop Boon, Thie SEQUENCES: DENCE ADDRESS	wolf, Greeon Atlantic ston	JA410 READABLE FORM: TYPE: Floppy ER: IBM PC CON ING SYSTEM: PC KG: PATENTIN F	APPLICATION NUMBER: US/O FILING DATE: CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Van Amsterdam, Joh REGISTRATION NUMBER: 40, REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATI	1: (617)720-250U 1: (617)720-2441 1: FOR SEQ ID NO: 7 CHARACTERISTICS: 4524 base pairs nucleic acid DNESS: double TY: linear TYPE: CDNA CAL: NO	.14	3.1%; llarity 47.3%; Conservative	aac - GAC	cgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: DELLAPORTA, STEPHEN L. TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patentin Release #1.0, Version #1.25
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3.0%; Score 42.2; DB 3;
Best Local Similarity 39.3%; Pred. No. 0.13;
Matches 152; Conservative 26; Mismatches 209;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVE. N.W.
CITY: WASHINGTON
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OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
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(202) 887-0763
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US-08-440-856A-9
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APPLICANT: BARR, PHILIP J
APPLICANT: KIEFER, MICHAEL C
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND
TITLE OF INVENTION: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS
NUMBER OF SEQUENCES: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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Pred. No. 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: NEELEY PH.D., RICHARD L. REGISTRATION NUMBER: 30092
REFERENCE/DOCKET NUMBER: CHIR-009/01US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1044 IWTCSGGCCACACCTYGTCGTSGACG 1070
                                                                                                                                                                                                                                                                                                                                                                                                602 gagtggaggacagtgtggactggaagg 628
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APPLICATION NUMBER: US/08/284,941
FILING DATE: 2 August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08284941
Patent No. 5863756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rioppy disk
compatible
OPERATING SYSTEM: Principle
SOFTWARE: Princ
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TELEFAX: (415) 857-0663
TELEX: 380816 COCLEY PA
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.9%;
Best Local Similarity 54.4%;
Matches 81; Conservative
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LENGTH: 4403 base pairs
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ADDRESSEE: COOLEY GO
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STATE: CALIFORNIA
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; LOCATION:
US-08-284-941-1
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824 gcgaaccgcggggcggagaccgagctcggggccggtgcggcgagctcaagcagttcc 883

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841 TGTGAACTGGAGCCCCC 858
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824 gcgaacgcgggggggggagagccgagctcggggcggtgcggcggcgagctcaagcagttcc 883
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APPLICANT: KIEFER, MICHAEL C
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND
TITLE OF INVENTION: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
STREET: FIVE PALO ALTO SQUARE
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Pred. No. 0.57;
0; Mismatches 68; Indels 0
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UNRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02147A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/848,629
FILING DATE: 09 HAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: NEELEY PH.D., RICHARD L
REGISTRATION UMBER: 30092
REFERENCE/DOCKET NUMBER: CHIR-009/00US
                                      884 tgggctggctcaagaagcacgcgtactgc 912
                                                                          165 GCGACAGGCTCGCGCGGCGCCCGAGCTGC 137
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                                                                                                                                RESULT 4
PCT-US93-02147A-1/c
; Sequence 1, Application PC/TUS9302147A
; GENERAL INFORMATION:
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Best Local Similarity 54.4%;
Matches 81; Conservative
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TELEX: 380816 COOLEY PA.
INPORMATION FOR SEQ ID NO: SEQUENCE CHARATTERISTICS:
LENGTH: 4403 base pairs
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MOLECULE TYPE: DNA (cDNA)
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STRANDEDNESS: double
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MEDIUM TYPE: Floppy
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LOCATION: 170..3077
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CALIFORNIA
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PCT-US93-02147A-1
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721 CCACTGCTGCATCCCACGCAAACACCTGCTGTTGTACCAGAATATGGGCATCTGGGTGCA 780
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                                                          APPLICANT: Nagata, Shigekazu
APPLICANT: Fukunaga, Rikiro
TITLE OF INVENTION: DNA Encoding Granulocyte
TITLE OF INVENTION: Colony-Stimulating Factor Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones, Tullar & Cooper, P.C.
STREET: P.O. Box 2266 Eads Station
                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 03-JUL.1990
FILING DATE: 03-JUL.1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCI/JP91/00375
FILING DATE: 22-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: RELIMENCE, James W.
REGISTRATION NUMBER: 28,808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74539/1990
FILING DATE: 23-WAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 176629/1990
                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARD.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,976
FTLING DATE: 19920922
                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Policies
Sequence 3, Application US/07923976
Patent No. 5574136
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Best Local Similarity 55.1%;
Matches 76; Conservative
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                                                                                                                                                                                                                                                                         STATE: Virginia
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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                                                                                                                                                                                                                                                          CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY:
; LOCATION:
US-07-923-976-3
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APPLICANT: Nagata, Shigekazu
APPLICANT: Fukunaga, Rikiro
TITLE OF INVENTION: DA Eccoding Granulocyte
TITLE OF INVENTION: Colony-Stimulating Factor Receptor
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                                                                                                AFTILE OF INVENTION: DNA Encoding Granulocyte TITLE OF INVENTION: Colony-Stimulating Facts NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: ADDRESSEE: Jones, Tullar & Cooper, P.C. STREET: P.O. Box 2266 Eads Station STATE: Virginia ZITY: Alington STATE: Virginia ZITY: Alington STATE: Virginia ZITE: 2202
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74539/1990
FILING DATE: 23-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JF 176629/1990
FILING DATE: 03-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCI/JP91/00375
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FILING DATE: 22-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
Application US/07923976
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REGISTRATION NUMBER: 28
REFERENCE/DOCKET NUMBER:
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Best Local Similarity 55.1
Matches 76; Conservative
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STRANDEDNESS: single
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US-07-923-976-7
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US-08-366-577-1
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                                                                                                                 APPLICANT: Nagata, Shigekazu
APPLICANT: Fukunaga, Rikiro
TITLE OF INVENTION: DNA Encoding Granulocyte
TITLE OF INVENTION: Colony-Stimulating Factor Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62;
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                                                                                                                                                                                                                        SSEE: Jones, Tullar & Cooper, P.C.
F: P.O. Box 2266 Eads Station
Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74539/1990
FILING DATE: 23-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 176629/1990
FILING DATE: 03-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCI/JP91/00375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/JP91/00375
FILING DATE: 22-MAR-1991
ATORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/07/923,976
FILING DATE: 19920922
                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                  Application US/07923976
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REGISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 51.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-415-1500
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Best Local Similarity 55.1°
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEIC ACID
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170..2482
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                                                                                                                                                                                              NUMBER OF SEQUENCES: 8
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CLASSIFICATION:
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STREET: P.C
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US-07-923-976-5
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US-07-923-976-7
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408 ggccaccaaccgcctgggctctgcccgctccgatgtactcacgctggatatcctggatgt 467
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                                                                                            348 ccactcotgccacatccccaaggacctggctctttacgccctatgagatctgggtgga 407
DB 1; Length 3024;
                                                Indels
                                                   0; Mismatches
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APPLICANT: KIGZIEF, Kenneth W.
TITLE OF INVENTION: POLYMERASE DELTA MUTATIONS IN COLORECTAL
TITLE OF INVENTION: TUMORS WITH REPLICATION ERRORS
NUMBER OF SEQUENCES:
ADDRESSPONDENCE ADDRESS:
ADDRESSE: Banner, Birch, McKie & Beckett
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                                                                                                                E: Banner, Birch, McKie & Beckett
1001 G Street N.W.
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0; Mismatches
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APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL CALCIUM-BINDING
TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.48554
                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/366,577
FILING DATE: 12-DEC-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                     IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08828242
Patent No. 5871970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          relecommunication information Telephone: 202-508-9100
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Best Local Similarity 51.1%;
Matches 90; Conservative (
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TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
EDNESS: double
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                                                                                                                                                 Washington
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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US-08-366-577-1
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GENERAL INFORMATION:
APPLICANT: VOGelatein, Bert
APPLICANT: Kinler, Kenneth W.
TITLE OF INVENTION: POLYMERASE DELTA MUTATIONS IN COLORECTAL
TITLE OF INVENTION: TUMORS WITH REPLICATION ERRORS
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                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastESOF for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,242
FILIG DATE: Filed Herewith
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3: Incyte Pharmaceuticals, Inc.
3174 Porter Drive
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1001 G Street N.W.
                                                                                                                                                      E: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELECOMMUNICATION INFORMAT
                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Billings, Lucy J
REGISTRATION NUMBER: 30
REFERENCE/DOCKET NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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INFORMATION FOR SEQ ID NO
                                                                                                                             COMPUTER READABLE FORM MEDIUM TYPE: Disket
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
           STREET: 31/7 CITY: Palo Alto
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Best Local Similarity
Matches 108; Conserv
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                                                                                       USA
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                                                                                                      94304
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                                                                                     COUNTRY:
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5296 GTCGGCAGGCCCCGGCGGAGGATGAAGTCGAGCAGCGGCAACTGCCGGTAGAACAGCGCG 6355
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APPLICANT: Tibbot, Brian K
TITLE OF INVENTION: Cloned Alpha-Glucosidase from Barley
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .0; Mismatches 143; Indels
PatentIn Release #1.0, Version #1.25
         29-AUG-1997
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                                                               FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : Pseudomonas aeruginosa,
Clinical Isolate P2-2
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STREET: 1 South Pinckney Street
CITY: Madison
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                                                                                                                                                                                                 NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,54
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Best Local Similarity 46.4%;
Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 9515 base pairs
                                                                                                                                                                                                                                                                                      312/474-6300
312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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US-08-920-812-13
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                                                                                      Patentin Release #1.0, Version #1.25
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Pred. No. 1.4;
0; Mismatches
                                    XY: United States of America 60606-6402
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                                                                                                                                                                                                                                        32,141
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APPLICANT: Matsuhlaa, Akio.
APPLICANT: Uchara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for
                                                                                                                                                                                                                    NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01
PELECOMMUNICATION INFORMATION
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 51.1%;
Matches 90; Conservative
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                                                                                                                                                                                                                                                                                                                                                   TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
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  COMPUTER READABLE FORM:
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43..3364
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Length 9515;

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TYPE: nucleic acid
STRANDEDNESS: double
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
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Matches 124; Conserva
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1621 ACACCGCTTACTGGACTGGCGACAACGCCGCAACGTGGGGCGACGTGCGCTACTCCATCA 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1741 TCAACGGCAACACACAGAGGAGCTCTGGGGTGGATCCAGCTCGGAGCCTTCTACC 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       551 caccegecteaaggattteetettteaagecaaataeeagateegetaeegagtggagg 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 491 acgigacacgigagccgcgicggggcciggaggaccagcigagcgigcgcigggigtcgc 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tggccggcctgaaacccggcaccgtgtacttcgtgcaagtgcgctgcaacccctttggca 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acagitgigaciggaaggiggiggacgaig----igagcaaccagacciccigcogcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3; Length 2752;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                             PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38.2; DB 3;
Pred. No. 1.5;
0; Mismatches 208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              845 cgagctcggggccggtgcggcgcgagctcaagc 877
                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296.93171
                                                                                     APPLICATION NUMBER: US/08/430,925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13, Application US/08920827
Patent No. 5770375
IBM PC compatible
                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Matsuhisa, Akio
APPLICANT: Uehara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.7%;
Best Local Similarity 45.5%;
Matches 179; Conservative
                                                                                                                                                                                                                                                                            TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                               URRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA
                    OPERATING SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                    linea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION:
US-08-430-925A-3
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6296 GTCGGCAGGCCCCGGCGGAGGATGAAGTCGAGCAGCGGCAACTGCCGGTAGAACAGCGCG 6355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6176 CAGGGCAGCTCTTCCAACACCCTGCAGATACCGACAGCCCTCGGTATCCAGCGCTGC 6235
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: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                   Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.4%; Pred. No. 2..,
tive 0; Mismatches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.7%; Score 38.2;
                                                                STATE: 1111fiols
COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1006 cctcgggcagacggggcacggcgagag 1032
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                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/362,577 FILING DATE: 27-MAR-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,827
FILING DATE: 29-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
STRAIN: Clinical Isolate P2-2
                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13, Application US/08921177
Patent No. 5798211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9515 base pairs
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Matsuhisa, Ak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312/474-0448
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INFORMATION FOR SEQ ID NO:
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Soji ON: Probe for Diagnosing Infectious Disease

Ohno, Tsuneya

3: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive

ADDRESSEE:

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APPLICANT: Eda, SOji
TITLE OF INVENTION: Pro
NUMBER OF SEQUENCES: 2:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 9515;
Probe for Diagnosing Infectious Disease
                                                                  S: Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/921,177
FILING DATE: 29-40G-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
FELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1006 cctcgggcagacggggcacggcgagag 1032
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                                                                                                                                                                COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
STRAIN: Clinical Isolate P2-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                    Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Sequence 13, Application US/08362577C Patent No. 5807673 GENERAL INFORMATION:

RESULT 15 US-08-362-577C-13

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6176 caececaecretrecaacaececrecaearacearaeceacaecerecres 6235
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                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/362.5777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: September 28, 1999, 16:40:56
Job time: 7042 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38.2;
Pred. No. 2
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                                                                                                                                                                                                                                               FILING DATE: 27-MAR-1995
CLASSIFICATION: 536
                                                           STATE: Illinois
COUNTRY: United States of America
IP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa STRAIN: Clinical Isolate P2-2 US-08-362-577C-13
                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.7%;
Best Local Similarity 46.4%;
Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9515 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
EDNESS: double
                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
STREET: boccorrections chicago
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29-OCT-1998

EST

ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

FEATURES

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qe50c05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
INAGE:1742408 3' similar to TR:Q16354 Q16354 PROLACTIN RECEPTOR ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: lung; Vector: p773D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Ist standfied polylinker; Site_1: Not I; Site_2: Eco RI; Ist standfied CDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTATATTTTTTTTTTTTTTTTT-3'] aduble-stranded CDNA was size selected, ligated to Eco RI the Not I and Eco RI sites of a modified p773 vector (Pharmacia), dispense de modified p773 vector (Pharmacia). Library went through one round of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbH119W."
                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbl.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: KOLLINGS TEL: (301) 496-1550
Email: Robert Strausbergenih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image:llnl.gov) for further information.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 477)

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                                                                                                                                                                                                                                                                                                                                                                                                                   On Feb 17, 1998 this sequence version replaced gi:2150926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_"IMAGE:1742408"
/clone_lib="Soares_fetal_lung_NbHL19W"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.1%; Score 307; DB 43;
99.7%; Pred. No. 9.5e-55;
tive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert Length: 1552 Std Error.
Seg primer: -400P from Gibco
High quality sequence stop: 467
Location/Qualifiers
                                                                                                                                                                    93736562
A1185924.1 GI:3736562
                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.7
Matches 307; Conservative
                                                                                                                                  mRNA sequence.
                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                 AI185924
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                                                                                                                                                                                                                                   human,
                                                                                DEFINITION
                                                                                                                                                                                                                                                ORGANISM
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ORIGIN
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AUTHORS
TITLE
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COMMENT
                   RESULT 1:
AI185924
LOCUS
                                                                                                                                               ACCESSION
                                                                                                                                                                                   VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOTTACCAATCREAAGTGGGAGCGCCGCATTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo."

110 c 104 g 80 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                    /Glone="IMAGE:1665990"
/Clone="IMAGE:1665990"
/Clone_lib="Soares_senescent_fibroblasts_NbHSF"
/tissue_type="senescent_fibroblast"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT7T3D (Pharmacia) with a modified
polylinker V_TYPE: phagemid; Site_1: Not I: Site_2: Eco
RI: lst strand cDNA was primed with a Not I - oligo(dT)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 364)

NCI-GAP http://www.ncbl.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergeinh.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1197 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 353.
Localin/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gggcacctgagccctcagcaggagctgggctggccctgagctccaacggccataacag 1192
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Pred. No. 4.6e-56;
0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                              1. .364
/organism="Homo sapiens"
/db_xref="taxon:9606"
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22.5%;
Best Local Similarity 94.5%;
Matches 346; Conservative
                                                                                                        Tumor Gene Index
Unpublished (1997)
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BASE COUNT ORIGIN

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1373

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Gaps

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Indels

Length 477;

us-09-037-657-24.rst

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RESULT 14
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                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                      normalization to a cot - 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           356 bp mRNA EST 16-FEB-1999 Soares_pregnant_uterus_NbHPU Homo saplens cDNA clone 50 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                 1270 ctagaacccctgccagggctgggggtgagaaggggagtcattactccccattacctaggg 1329
                                                                                                                                                                                                                                                                                                                                                                                                                                1091 aggocgaacccaaactggggccacctctgtaccctcacttcagggcacctgagc.ccctc 1149
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 356)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 37; Length 394;
                                                                                                                                                                                                                                                                                                                                  Score 326.6; DB 37; Length Pred. No. 7.5e-59; 0; Mismatches 4; Indels
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                                                                                       clone_lib="Soares_fetal_heart_NDHH19W"
'sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primer: -40ml3 fwd. ET from Amersham
                                               organism-"Homo sapiens"
/db_xref="GDB:1288024"
/db_xref="taxon:9606"
/clone="IMAGE:379768"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:4175774
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Best Local Similarity 98.6%;
Matches 340; Conservative (
                                                                                                                                                                                                                                                                           NDHL19W."
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IMAGE:2042750 3'
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AI375784/c
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oy16c04.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1665990 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                occoagtagatatatatatatatataaagattagtttaatttgactagaaccoctgocagg 1286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ggccacctctgtaccctcacttcagggcacctgagc.-ccctcagcaggagctggggtgg 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   occotgagotecaacggccataacagotetgaeteccaegtgaggccaeetttgggtgca 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          356 TGTAGGGGCTCAGGCCACCTCCCTGCCACGTGGAGACGCAAAGGCCGAACCCAAACTGG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 ccccrgagcrccaacgccaraacagcrrrgacrcccacgrgaggccaccrrrgggrgca 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
On Apr 3, 1998 this sequence version replaced gi:3017967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 356;
                                                                      Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550
Email: Robert_Strausberg@hih.gov
This clone is available royalty-free through LLNL
INAGE Consortium (info@image.llnl.gov) for further
finsert Length: 1238 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop: 307.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 321.4; DB 45; Length
Pred. No. 8.9e-58;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:2042750"
/clone_llb="Soares_pregnant_uterus_NbHPU"

    .356
    /organism="Homo sapiens"
    /db_xref="taxon:9606"

                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:3423630
                                                                                                                                                                                                                                                                                                                                                                    /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 23.1%;
Best Local Similarity 97.7%;
Matches 337; Conservative
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AA706010/c
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AUTHORS
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2V11e07.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:753348
3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:753348"
/clone_11b="Soares_NhHMPu_S1"
/tlssue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
7el: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
Fhis clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
High quality sequence stop: 422.
                                                                                                                                                             549
                                                                                                                                                                                                                                                            caggacaacacatgtgaggagtaccacacagtggggccccactcctgccacatccccaag 369
                                                   gacciggcicititacgccctatgagatcigggiggaggccaccaaccgcctgggcict 429
                                                               489
                                                                                                                   133 GCGAGATCTGACGTGCTCACACTGGATGTCCTGGACGTGGTGACCACGGACCTCCACCC 192
                                                                                                                                                                    550 ccacccgcctcaaggatttcctctttcaagccaaataccagatccgctaccgagtggag 609
                                                                                                                                                                                                                                 253 ccaccagcrercaaggarricererrecaagecaaaraceagarregeracegergsag 312
                /lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
                                                                                                     gccgctccgatgtactcacgctggatatcctggatgtggtgaccacggacccccgccc
                                                                                                                                                      490 gacgtgcacgtgagccgcgtcggggcctggaggaccagctgagcgtgcgctggttgt

    433
    /organism="Homo sapiens'
/db_xref="GDB:5976201"
    /db_xref="taxon:9606"

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AA406406.1 GI:2064592
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AA406406/c
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(Pharmacia) with a modified polylinker; Site_1: Not I; Stle_2: Eco RI: Equal amounts of plasmid DNA from three normalized libraries (melanocyte ZNBHW, pregnant uterus NDHPU, and fetal heart NDHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization fraction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools of consisted of I.M.A.G.E. clones 260232-265223, and 484488.489479."
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Tel: 314 286 1810
Fax: 314 286 1810
Bmail: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutharia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 394)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylle,T., Waterston,R. and Wilson,R. Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                286
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                                                                                                                                                                                                                                                                                                                                                                                                        1031 aggtoctgecagataagctgtaggggtcaggccacctccctgccacgtggagacgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1091 aggoogaacccaaactggggccacctctgtaccctcacttcagggcacctgagc--ccct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1149 cagcaggagetgggtggccctgagetccaacggccataacagetetgaeteccaegtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  285 AGGCGAACCCAAACTGGGGCCACCTCTGTACCTCACTTCAGGGCACCTGAGCCACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 327.8; DB 33; Length 433;
Pred. No. 4.3e-59;
0; Mismatches 2; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On May 8, 1995 this sequence version replaced gi:801325
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Washington University School of Medicine
Mashington True Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            zf44a09.s1 Soares_fetal_heart_NbHH19W Homo
IMAGE:379768 3', mRNA sequence.
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AA706010.1 GI:2715928
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ilarity 98.8%;
Conservative
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1279 ctgccagggctgggggtgagaaggggagtcattactccccattacctagggcccctccaa 1338
158 reserceceaereserererererererereaeserreserereaerrecerasaaece
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Best Local Similarity 87.7%;
Matches 365; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 415)
NCI-CGAP http://www.ncbl.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1466 Std Error: 0.00 Seq primer: -40ml3 fwd. Er from Amersham High quality sequence stop: 403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA992638 415 bp mRNA EST 27-AUG-1998 ot81b10.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1623163313', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        981 ccagcacaggacgaggggatcctgccctcgggcagacgggggacgggggagggtcctgcc 1040
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Pred. No. 1.2e-65;
0; Mismatches 8; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1623163"
/clone_lib="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                            AA992638.1 GI:3178372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 97.2%;
Matches 387; Conservative
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Unpublished (1997)
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/map="between D118176-04-0-UI"
/clone="tu-R-A0-1f-04-0-UI"
/dev_stage="dawle"
/dev_stage="dawle"
/lab_host="bH108 (life Technologies)"
/note="vector: pT73D-Pac (Pharmacia) with a modified
polyplinker; Site_1: Not I; Site_2: ECO RI; This library
consists of a mixture of individually tagged normalized
libraries constructed from rat placenta, adult lung,
brain, liver, kidney, heart, spleen, ovary, and muscle.
The tag is a string of 3.5 nucleotides present between the
Not I site and the oligo-dT track which allows
identification of the library of origin of a clone within
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Fax: 319 335 9565
Fax: 319 335 9565
Fax: 319 335 9665
Fax: 319 335 9666
Fax: 319 335 9666
Fax: 319 3666
Fax: 319 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 310 Fax: 3
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
I (bases 1 to 428)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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98 CIGCCAGGGCTGGGGGTGAGATAGGGAGTCATTACTCCCCATTACCTAGGGCCCCTCCAA 39
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Pred. No. 1.8e-60;
0; Mismatches 51; Indels 0;
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    .428
    /organism="Rattus norvegicus"

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us-09-037-657-24.rst

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/note="Organ: 1900 of vector: p1773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-72871, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. " Subtraction by Bento
                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergénih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1117 Std Error: 0.00
Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 358.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1052 aggggctcaggccacctccctgccacgtggagacgcagaggccgaacccaaactggggc 1111
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1 (Dases 1 to 394)
NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap,
National Cancer Institute, Cancer Genome Anatomy Project (CGAI Tumor Gene Index
Unpublished (1997)
On Jan 17, 1998 this sequence version replaced gi:2044794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              932 tctacgaccagtggcgagcctggatgcagaagtcgcacaagacccgcaaccagcacagga 991
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Pred. No. 5.1e-67;
0; Mismatches 2; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                  1. .394
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/clone="InAGE:152230"
/clone_11b="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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                               Homo saptens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ccgcccgacgtgcacgtgagccgcgtcgggggcctggaggaccagctgagcgtgg
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                                                                   /map="10 pter-cen"
/clone="IMAGE:387741"
/clone_11b="Soares mouse embryo NbME13.5 14.5"
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//dev_stage="13.5-14.5dpc total fetus" | /lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 26.5%; Score 368.4; DB 26; Best Local Similarity 87.9%; Pred. No. 1.5e-67; Matches 413; Conservative 0; Mismatches 56;
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                    /organism-"Mus musculus"
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Matches 386;
                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reaction. The driver was PCR-amplified cDNAs from pools of 5.000 clones made from the same 3 libraries. The pools consisted of I.M.A.G. E. clones 260232-265223, 340488-345479, and 484488-489479.
                                                                                                                                                                                                                                                                                                                                                                                                           A1417616 389 bp mRNA EST 30-MAR-1999 tg80c02.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2115074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:2115074"
/clone_lib="Soares_NhHWPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the TMAGE Consortium (info@image.llnl.gov) for further information.
INAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -400P from Gibco
High quality sequence stop: 383.
Location/qualifiers
1. 389
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                             1277 ccctgccagggctgggggtgagaaggggagtcattactccccattacctagggcccctcc 1336
                                338 CCAGATAAGCTGTAGGGGCTCAGGCCACCCTCCCTGCCACGTGGAGACGCAGAGGCCGAA 279
                                                                                                                                                                                                                                                 98 CCCTGCCAGGGCTGGGGGTGAGAAGGGAAGTCATTACTCCCCATTACCTAGGGCCCCTCC 39
                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 389)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On May 7, 1998 this sequence version replaced gi:3120565.
                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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AI417616.1 GI:4261120
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Unpublished (1997)
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BASE COUNT ORIGIN

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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 483.)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                                                                                                                                                  987 caggacgagggatcctgccctcgggcagacggggcacggcgagagggtcctgccagataa 1046
                                                                                                                                                                                                    gotgtaggggotcaggccacctccctgccacgtggagacgcagaggccgaacccaaact 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        caccccagtgggtgtgtgtgtgtgtgtgtgagggttgagttgagttgctagcaaccctgcca 1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gggctgggggtgagaaggggagtcattactcccattacctagggccctccaaaagagt 1344
                                                                                                                                                                                                                                                                                                                                                                                                     ggcccttgagctccaacggccataacagctctgactcccacgtgaggccacctttgggtg 1224
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                                                                                                                                89 GGGCTGGGGGTGAAAGGGGAGTCATTACTCCCCATTACCTAGGGCCCCTCCAAAAGAGT 30
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Unpublished (1996)
On Apr 14, 1993 this sequence version replaced g1:785250
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Length 389
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Seg primer: ETPrimer
High quality sequence stop: 359.
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WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                    Indels
  DB 46;
                          Pred. No. 1.3e-68;
0; Mismatches 1
  26.8%; Score 373.4; 99.2%; Pred. No. 1.3
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W66776.1 GI:1375694
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Homo saptens
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A1264328/c
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                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:289787
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 437.
Location/Qualifiers
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 Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                               Unpublished (1996)
On Dec 30, 1996 this sequence version replaced 91:1528951
                                                                                                                                           WashU-HHMI Mouse EST Project WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:479043"
/clone_lib="Soares mouse embryo NbME13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 380.8; DB 29; Length 464;
Pred. No. 4e-70;
0; Mismatches 52; indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
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t
                                                                                                                            Contact: Marra M/Mouse EST Project

    464
    /organism="Mus musculus"

                                                Waterston, R.
The WashU-HHMI Mouse EST Project
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Kucaba,T., Lacy,M.
rg,K., Steptoe,M.,
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Best Local Similarity 88.8%;
Matches 412; Conservative (
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Fax: 314 286 1810
Email: moneon
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/note="Organ: mixed (see below); vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI: Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-385479. "8 4 a 123 c 117 g 84 t
                                                                                                                                                                                                                                                                                                                                   AI264328 398 bp mRNA EST 27-JAN-1999
q109c05.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1855976
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Soares_NhHWPu_si"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 699 Std Error: 0.00
301 ACGTGAGCCGCGTTGGGGGCCTGGAGGACCAGCTGAGTGTGCGCTGGGTCTCACCACCAG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         979 aaccagcacaggacgaggggatcctgccctcgggcagacggggcacggcgagagtcctg 1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                               557 ccctcaaggatttcctctttcaagccaaataccagatccgctaccgagtggagggcagtg
                                                                               Tumor Gene Index
Unpublished (1997)
On Jan 14, 1998 this sequence version replaced g1:1797852.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebra
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 398)
                                                                                                                                              Score 380.8; DB 4.
Pred. No. 3.9e-70;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nlh.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: -400p rrow size High quality sequence stop: 397 Location/Qualifiers 1.398 .....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:1855976"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
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Query Match

BASE COUNT ORIGIN

Local

Matches

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1123

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AA049280 464 bp mRNA EST 30-DEC-1996 mj45d02.rl Soares mouse embryo NDME13.5 14.5 Mus musculus CDNA clone IMAGE:479043 5' similar to SW:ILGB_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 464)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
                                                             Anote—"Organ: pooled; vector: pT7T3D-Pac (Pharmacia) with model—"Organ: pooled; vector: pT7T3D-Pac (Pharmacia) with modified polylinker; Sited—1: Not I: Sited—2: ECO RI: Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_GAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made Irom the same 3 libraries. The pools consisted of Irom the same 3 libraries. The pools consisted of Irom the same 3 libraries. The pools consisted of Irom the and 3 libraries. The pools consisted of Irom the and 3 libraries. The pools consisted of Irom the and 3 libraries. The pools consisted of Irom the and 3 libraries. The pools consisted of Irom the and 3 libraries. The pools consisted of Irom the and 3 libraries. The pools consisted of Irom the and 3 libraries. The pools consisted of Irom the and 3 libraries. The pools consisted of Irom the and 3 libraries. The pools consisted of Irom the and 3 libraries. The pools consisted of Irom the and 3 libraries. The pools consisted of Irom the and 3 libraries.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gagccctcagcaggagctggggtggccctgagctccaacggccataacagctctgact 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          963 gtcgcacaagacccgcaaccagcacaggacgaggggatcctgccctcgggcagacggggc 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295 AGACGCAGAGGCCGAACCCAAACTGGGGCCACCTCTGTACCCTCACTTCAGGGCACTCTG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metazoa, Chordata, Craniata, Vertebrata, Mammalia)
Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         410 GICGCACAAGACCCGCAAC----CAGGACGAGGGGATICCTCCCTCGGGCAGAGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agacgcagaggccgaacccaaactggggccacctctgtaccctcacttcagggca--cct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 NACACCCTCAGCAGGAGCT-GGGTGGCCCCTGAGCTCCAACGGCCATAACAGCTCTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                           Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                               Score 394.8; DB 40;
Pred. No. 4.9e-73;
0; Mismatches 8;
                       /clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                              Soares and M. Fatima Bonaldo.
139 c 142 g 100 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:1755311
                                                                                                                                                                                                                                                                                                                                                                                               28.4%;
illarity 96.2%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 459; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eutheria;
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KEYWORDS
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Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (linfo@limage.llnl.gov) for further information.
Insert Length: 763 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 448.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbl.nlm.nlh.gov/nclogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                     1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1182 ggccataacagctctgactcccacgtgaggccacctttgggtgcaccccagtgggtgtgt 1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 geccaraacaecrereacreceaegreaececaecrireeerecaececeaeregerer 133
                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 469)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA922128 469 bp mRNA EST 23-JUN-1998
om45e12.s1 Soares_NPL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1544014 3', mRNA sequence.
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             943 tggcgagcctggatgcagaagtcgcaaagaccgcaaccagcacaggacgaggggatcc
                                                                                                                                                                                                                                           1003 tgcctcgggcagacgggcacggcgaggtcctgccagataagctgtaggggctcagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On May 8, 1995 this sequence version replaced g1:800381.
                                                                                                                    .;
7
                                                                              Length 431;
                                                                            Score 406.4; DB 28; Length
Pred. No. 1.8e-75;
0; Mismatches 1; Indels
16
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
    Б
  129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA922128.1 GI:3069437
                                                                                29.2%;
99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index
Unpublished (1997)
    O
                                                                                                                        429; Conservative
  134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                       Similarity
      ๙
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FEATURES

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

LOCUS DEFINITION RESULT 3 AA922128/c

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us-09-037-657-24.rst

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/organism="Homo sapiens"
/db_xref="GDB:3804591"
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lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and Marra, M.
                                                                                                                                                                                                                                                                                                   RESULT 2
AA121532/c
                                                                                                                                                                                                                                                                                                                                                  DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ñ
                                                              Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             caagacccgcaaccagcacaggacgagggatcctgccctcgggcagacg-gggcacggc 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cagaggoogaacccaaactggggocacctctgtaccctcacttcagggcacctgagc--c 1145
                                                                                                                                                                                                                                                                                                                                                                                                            th LLNL ; contact the further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CTGCTCCAACCTCCAGCTTCCGCCTCTACGACCAGTGGCGAAGCCTGGATGCAGAAGTCGCA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           909 ctgctccaacctcagcttccgcctctacgaccagtggcgagcctggatgcagtagtcgca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Sep 12, 1996 this sequence version replaced gi:1393691
                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louls, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 425.4; DB 29; Length 467;
Pred. No. 2.1e-79;
0; Mismatches 4; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAAGAATTCGCGGCCGTTTTTTTTTTTTTTT 3']
                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL IMAGE Consortium (info@image.llnl.gov) for further putative full length read
The vector to vector length is 468
Insert Length: 542 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Soares_pregnant_uterus_NbHPU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             constructed by M. Fatima Bonaldo."
144 c 139 g 84 t 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo saplens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="GDB:3804591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lone-"IMAGE: 490004"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606
                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host-"DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match . 30.6%;
Best Local Similarity 98.3%;
Matches 460; Conservative
                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
                                    Homo sapiens
                                                                                                                                                                                                     and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96
KEYWORDS
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ORIGIN
                                                                                                                                                                                                                 TITLE
JOURNAL
MEDLINE
COMMENT
                                                                                 REFERENCE
                                                                                                  AUTHORS
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FEATURES

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1 (bases 1 to 431)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,M., Le,M.
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.
Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 11-MAY-1997 IMAGE: 490004 3', mRNA sequence. IMAGE: 490004 3', mRNA sequence.
1146 cctcagcaggagctggggtggccctgagctccaacggccataacagctctgactccac 1205
                                                                                                 1206 gigaggccaccttigggigcacccagigggigigigigigigigigggggitggitgag 1265
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 542 Export: 0.00
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 405.
Location/Qualifiers
                                                                                                                                                                                                                                          /note-"Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I Site_2: Eco RI; 1st strand cDNA was primed with a Not oligo(dT) primer [5'
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                              241 CCTCAGCAGGAGCTGGGGTGGCCCCTGAGCTCCAACGGCCATAACAGCTCTGACTCCCAC
                                                                                                                               Generation and analysis of 280,000 human expressed sequence Genome Res. 6 (9), 807-828 (1996)
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                              /clone="IMAGE:490004"
/clone_llb="Soares_pregnant_uterus_NbHPU"
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constructed by M. Fatima Bonaldo.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

AA127694 467 bp mRNA EST Zk89c11.r1 Soares_pregnant_uterus_NbHPU Homo IMAGE:490004 5', mRNA sequence. AA127694 g1686983 AA127694.1 GI:1686983	94 467 bp mRNA EST 11. 1.rl Soares_pregnant_uterus_NbHPU Homo sapiens 1900004 5', mRNA sequence. 94 94.1 GI:1686983	467 bp mRNA 1 Soares_pregnant_uterus_NbHPU)004 5', mRNA sequence. 1 GI:1686983
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	11. sapiens	11-MAY-1 sapiens cDNA

301 tggtatgg 308 |||||||| 470 TGGTATGG 477

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Search completed: September 28, 1999, 15:38:23 Job time: 3291 sec

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(bases 1 to 179436)

Zhan,G. Lao,V., Zhan,M. and Roe,B.A.

Direct Submission

Submitted (06-NOV-1997) Department Of Chemistry And Blochemistry,

The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                          337 tatttgattttatgaaaatatacctgtttgtatttggtttggtttggtttgagttttgtt 396
                                                                                                                                                                   457 aggctggccttgaactcagaaatccgcctgcttgtgcttcccaagtgcttagattaaagg 516
                                                                                                                                                                                                                                                                                                                                                                                                       AC003066 179436 bp DNA HTG 21-MAY-1999
Mus musculus chromosome 16 clone tbx1, WORKING DRAFT SEQUENCE,
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 179436)
Zhang, G. and Roe, B.A.
Mouse Chromosome 16 BAC Clone tbx1
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* NOTE: This is a 'working draft' sequence. It currently 'consists of 5 contigs. The true order of the pieces 's not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as soon as it is available and the accession number will be preserved
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                                                  Length 91638;
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88686: contig of 65216 bp in length
88778: gap of unknown length
179436: contig of 90658 bp in length.
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3222: gap of unknown length
8281: contig of 5059 bp in length
8373: gap of unknown length
3378: contig of 15005 bp in length
                                              Score 123; DB 34;
Pred. No. 1.2e-19;
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C hases I to 179436)
Emanuel,B. and Budarf,M.
Mouse Chromosome 16 BAC Clone tbx1
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/db_xref="taxon:10090"
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Unpublished (1997)

E 3 (bases 1 to 39061)

S Zhang,G., LaO., L., Zhan,M. and Roe,B.A.

S Zhang,G., LaO., L., Zhan,M. and Roe,B.A.

Direct Submission

Submitted (06-NOV-1997) Department of Chemistry And Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA

ON C4 31, 1998 this sequence version replaced gi:3132482.

* NOTE: This is a 'working draft' sequence. It currently
consists of 7 contigs. The true order of the pieces
consists of 7 contigs. The true order of the pieces
is not known and their order in this sequence record is
runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339 tttgattttatgaaaatatacctgtttgtatttggtttggtttggtttggtttgagtttgttta 398
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 39061)
                                                                                                                                                                                                                  Score 122; DB 35; Length 179436;
Pred, No. 2.1e-19;
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Emanuel, B. and Budarf, M.
Mouse Chromosome 16 BAC Clone tbx3
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Hawkins, T.L., Birren, B.W., Fasman, K.H., Nussbaum, C., Lander, E.S., McKernan, K., Murro, C., Richardson, P., Barna, N., Chang, A., Cooke, P., Dally, M.J., Devon, K., Dewar, K., Forrest, C., Gage, D., Geraigery, K., Hagos, B., Huang, J., Jacotot, L., Kirby, A., Lane, M., Mackenzie, J., Marquis, N., McDermott, J., Molla, M., Morrow, J., Nachman, A., Naylor, Nusbaum, C., O'Connor, T., Olotu, A., Stone, C., Strickland, C., Sydney, K., Tang, L., Wilmer, F., Zemtseva, I.
                               AC002489 91638 bp DNA HTG 20-JAN-1998
Homo sapiens chromosome X clone 592 map X, WORKING DRAFT SEQUENCE,
g unordered pieces,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (22-AUG-1997) Whitehead Institute/MIT Center for Genome Submitted (22-AUG-1997) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jan 20, 1998 this sequence version replaced 91:2772532.

The Staden databases, finishing information, and all chromatographic files used in the assembly of this clone are available from our anonymous ftp site.
                                                                                                                                                                                                                                                            ., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker.html.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 8 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N. but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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unknown length
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Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 91638)
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25406 a 19091 c 18992 g 28011 t
                                                                                                                                                                                                                                                                                             Homo sapiens chromosome X, clone 592
Unpublished
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Location/Qualifiers
1. .91638 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="592" /clone="11b="unknown"
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Pred. No. 8.7e-20;
0; Mismatches 34; Indels 1; G
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GSILAGSCLYVGLPPERPVNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWY
GODNTCEEPHTVGPHSCHIPKDLALFTPYEIWYBATNRLGSARSDVLTLDLUCVYTTD
PPPDVHYSRVGGLEDOLSVRWYSPPALKDFLEQAKYOIRYRVBDSVDMKVVDDVSNQT
SCRLAGLKPGTVYFVQVRCNPFGIYĞSKKAĞINSEWSHPTAASTPRSERPGRGGGACE
PRGGEPESSGPYRRELKÇFLGWLKKHAYCSNLSFRLYDQWRAWNQKSHKTRNQHRTRGS
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NICOLA NICOS ANTONY (AU)
LOCATION/QUALIFIERS
1. 5560
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Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S.,
Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
Kikuchi,Y.
                                                                                                                                                                                                                                                                                                    3673
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                                                                                                                                                                                                                                                                                    68;
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Pred. No. 3e-36;
0; Mismatches. 37;
                                 /note="unnamed protein product"
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/protein_id="cAB4276.1"
/db_xref="pID=1433703"
/db_xref="PID=94774673"
/db_xref="GI:4774673"
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organism="unidentified"
      /db_xref="taxon:32644"<1. .1053
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Best Local Similarity 73.5%;
Matches 291; Conservative (
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Dipublished

2 (bases 1 to 170965)

3 Hua,A and Roce,B.A.

Direct Submission

3 University of Oklahoma, 620 Parrington Oval, Room 208, Norman, Ok 73019, USA

On Jun 4, 1999 this sequence version replaced gi:4895262.

* NOTE: This is a 'working draft' sequence. It currently consists of 33 configs. The true order of the pieces

* arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                   3494 ctgagtgtgcgčtgggtctcaccaccagctctcaaggatttcctctccaagccaagtac 3553
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Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 170965)
Hua, A. and Roe, B.A.
Mus musculus Clone p481n4
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Mus musculus, WORKING DRAFT SEQUENCE, 33 unordered pleces
AC005302
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                                                                                                                DB 5; .Length 560;
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gap of unknown length
contig of 3125 bp in length
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                                                                                                            Score 141.2; DB 5
Pred. No. 4.1e-24;
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Best Local Similarity 92.08;
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Elson, G.C.A., Graber, P., Losberger, P., Herren, S., Gretener, D., Menoud, L.N., Wells, T.N.C., Kosco-Vilbols, M.H. and Gauchat, J.F. CLF-1, a Novel Soluble Protein Shares Homology With Members of Cyrokine Type-I Receptor Family J. Immunol. (1998) In press
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
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Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,
Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
Kikuchi,Y.
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/protein_id="AAC28335.1"
/db_xref="PID:g3372627"
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/note="similar to cytokine type-1 similar to the sequence presented
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llarity 86.5%; Pred. No. 1.9e-43;
Conservative 0; Mismatches .38
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4.2%; Score 280.4; DB 5;
Best Local Similarity 99.6%; Pred. No. 3.4e-58;
Matches 281; Conservative 0; Mismatches 1;
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/db_xref-"taxon:32644"
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                               18474 cccccccrcracrcracrrsrccrcacrcracragacarcaracarcaracaracaracras
                                                          1 (bases 1 to 1629)
Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S.,
Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
Kikuchi,Y.
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Best Local Similarity 99.6%; Pred. No. 3.4e-58;
Matches 281; Conservative 0; Mismatches 1
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Sequence 12 from Patent WO9811225.
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A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME PATENT: WO 9811225-A 19-MAR-1998; NICOLA NICOS ANTONY (AU)
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    (bases 1 to 1673)
    Nicola, N.A., Fabri, L., Farley, A., Nash, A., Willson, T., Rakar, S.,
    Zhang, J., Alexander, W., Hilton, D.J., Kojima, T., Maeda, M. and

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15713. .15760

// note="DDS similarity to AA121532 zk89c11.s1 Soares
pregnant uterus NDHPU Homo sapiens cDRA clone 490004 3'
(389. .343); 99% identity.--DS similarity to AA127694
zk89c11.r1 Soares pregnant uterus NDHPU Homo sapiens cDNA
clone 490004 5' (77. .125); 90% identity.--(15735. .15713)
DDS similarity to W46603 zc22hl0.r1 Soares senescent
fibroblasts NDHSF Homo sapiens cDNA clone 324067 5'
(351. .329); 100% identity.--(15735. .15713) DDS similarity
to W46604 zc32hl0.s1 Soares senescent fibroblasts NDHSF
Homo sapiens cDNA clone 324067 3' (299. .321); 100%
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complement(18270. .18438)

/note="predicted exon, program: grail2exons_human_1.3,
frame: 0, quality: excellent, score:
100.000--(18438. .18284) DDS.similarity to W66776
mel7blirl Scares mouse embryo NbWE13.5 14.5 Mus musculus
cDNA clone 387741 5' similar to PIR:B3825 ab3825
granulocyte colony-stimulating factor receptor precursor
(157. .1); 82% identity.--(18438. .18406) DDS similarity to
AA049380 m454602.r1 Scares mouse embryo NbWE13.5 14.5 Mus
musculus cDNA clone 479043 5' similar to SW:IL6B_MOUSE
Q00560 INTERLEUKIN-6 RECEPTOR BETA PRECURSOSR (432. .464);
88% identity."
                                    frame: 2, quality: Good, regress 6:1000--Other overlapping matches: (13756. 13875) DDS similarity to AA009412 zed2h02.r1 Soares fetal beart NDHH19W Home sapiens CDNA clone 36523 5′ (428. 496); 97% identity.--(13756. 13984) DDS similarity to AA009693 zed2h02.s1 Soares fetal heart NDHH19W Home sapiens CDNA clone 365523 3′ (227. 11); 98% identity.--(13756. 13984) DDS similarity to AA460010 zx33f04.s1 Soares total fetus NDZHF8 9w Home sapiens CDNA clone 365523 3′ (227. 11); 98% identity.--(13756. 13984) DDS similarity to AA460010 zx33f04.s1 Soares total fetus NDZHF8 9w Home sapiens CDNA clone 788287 3′ (228. 1); 99% identity.-"

Intelly="Alu" | 198% identity.-"

Intelly="DDS similarity to AA406406 zv11e07.s1 Soares NHHMPU S1 Home sapiens CDNA clone 753348 3′ (1. 433); Score: 858 identity: 4212402.r1 Soares fetal lung NDHL19W Home sapiens CDNA clone 302666 5′ (1. 355); 94% identity.--(15227. 14885) DDS similarity to AA121522 zk89c11.s1 Soares pregnant uterus NDHPU Home sapiens CDNA clone 30266 5′ (1. 355); 94% identity.--(15227. 14885) DDS similarity to M46603 zc32h10.r1 Soares pregnant uterus NDHPU Home sapiens cDNA clone 490004 3′ (32. 1); 99% identity.--(15227. 14887) DDS similarity to W46603 zc32h10.r1 Soares senescent fibroblasts NDHSF Home sapiens cDNA clone 324067 5′ (328. 11); 99% identity.--(15227. 14897) DDS similarity to W46603 zc32h10.r1 Soares senescent fibroblasts NDHSF Home sapiens cDNA clone 324067 5′ (328. 13); 96% identity.--(15227. 15089) DDS similarity to W46603 cDNA clone 324067 3′ (322. 465); 96% identity.--(15227. 15227. 15089) DDS similarity to W46603 cDNA clone 324067 3′ (322. 465); 96% identity.--(15227. 15227. 15227. 15000 cDNA clone 324067 3′ (322. 465); 96% identity.--(15227. 15227. 15000 cDNA clone 324067 3′ (322. 465); 96% identity.--(15227. 15000 cDNA clone 324067 3′ (322. 465); 96% identity.--(15227. 15000 cDNA clone 324067 3′ (322. 465); 96% identity.--(15227. 465); 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .16082)
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frame: 1, quality: excellent, score: 100,000--DDS.
similarity to AA047548 zf15e0z.rl Scares fetal heart
NbHH19W Homo sapiens CDNA clone 377018 5' (139. '221); 100%
identity. --DDS similarity to AA136115 zk90b04.rl Scares
pregnant uterus NbHpU Homo sapiens CDNA clone 49063 5'
(111. 192); 99% identity. --DDS similarity to AA452628
zx33f04.rl Scares total fetus ND2HF9 by Homo sapiens CDNA
clone 788287 5' (83. .165); 100% identity. --DDS similarity
to AA009412 ze82h02.rl Scares fetal heart NbHH19W Homo
sapiens cDNA clone 365523 5' (62. .144); 100% identity."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heart NDHH19W Homo sapiens cDNA clone 377018 5' (1. .138); 96% identity. --Other overlapping matches:-(10435, .10548) DDS similarity to AA136115 zk90b04.r1 soares pregnant uterus NDHPU Homo sapiens cDNA clone 490063 5' (1. .110); 93% identity. --(10466, .10548) DDS similarity to AA452628 zx33f04.r1 soares total fetus ND2HF8 9W Homo sapiens cDNA clone 788287 5' (1. .82); 95% identity. --(10486, .10548) DDS similarity to AA009412 ze82h02.r1 soares fetal heart NDHH19W Homo sapiens cDNA clone 385523 5' (1. .61); 97%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anote-"DDS similarity to AA136115 zk90b04.rl Soares pregnant uterus NbHPU Home sapiens cDNA clone 490063 5/ (395, 477); 92% identity. -DDS similarity to AA009412 ze82h02.rl Soares fetal heart NbHH19W Home sapiens cDNA clone 365523 5/ (347, 427); 94% identity. -DDS similarity sapiens cDNA clone 365523 3/ (306, 228); 99% identity. -DDS similarity to AA096012 ze32h19 identity coarses fetal heart NbHH19W Home sapiens cDNA clone 365523 3/ (306, 228); 99% identity. -DDS similarity to AA450010 zx33f04.sl Soares
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="predicted exon, program: grail2exons_human_1.3,
frame: 1, quality: excellent, score: 75.000"
/rpt_family="ALU"
                                                                                                                                                                                                                                                                                                            complement(9445. .9505)
/note="predicted exon, program: grail2exons_human_1.3,
facture: 1, quality: good, score: 63.000"
complement(9629. .9672)
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complement(12966. .13240)
/rpt_family-"Alu"
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complement(11869. .12161)
/rpt_family="Alu"
12502. .12581
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family="Alu"
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rpt_family="Alu"
951. .905,
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9358. 9535
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Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S.,
Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
Kikuchi,Y.
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                                                                                                                                                                                                                                                                                                                       Length 1930;
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Pred. No. 2e-170;
0; Mismatches 27;
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Lamerdin, J.E., McCready, P.M., Adamson, A.W., Burkhart-Schultz, K.,
Gordon, L., Christensen, M., Kyle, A., Ramirez, M., Stilwagen, S.,
Garnes, J., Danganan, L., Bruce, R., Quan, G., Montgomery, M., Ow, D.,
Robayashi, A., Olsen, A.O. and Carrano, A.V.
Sequence analysis of an -1 Mb region containing the MEF2B gene in
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Direct Submission
Submitted (21-NOV-1997) Human Genome Center, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA Location/Qualifiers
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Eutheria, Primates, Catarrhini, Hominidae, Homo.
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QΥ	4872	ccagcaggcggctgcgtccgcccgagagactga	4931
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ζō	93	ggtaagcaggggctgtgggggccgaagttgtgccagggcctgtcagcgagtccccagtt	991
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Jtcacaci 	07-MAY Willson,T., R	SEQUENCES . Length . Indels	tgtgtttctaggtaat 	agatttga
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tggtcca - - - - -			:aagacag 	ggatgtal
acagctt. 	DNA WO9811 Farley,	EMOPOIETIN RECEPTOR AND GE 9811225-A 19-MAR-1998; OCA MINON' (AU) OCATION/QUALIFIERS .11832 Organism="unidentified" db_xref="taxon:32644" 3367 c 3298 g 2720 t 3367 c 3298 g 2720 t	Dangtttc	attaatad ATTAATAO LTALLTGI IIIIIII TTATTTGI
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	A70408 11832 bp Sequence 38 from Pater A70408 94774683 A70408.1 GI:4774683 unidentified unidentified unidentified unidentified logassified logassified logassified Loses 1 to 11832) Nicola.N.A., Fabri,L., Zhang,J., Alexander,W.	A NOVEL HAEMOPOLETIN RECEPTOR AND JOURNAL PATENT: WO 9811225-A 19-MAR-1998; NICCLA NICOS ANTONY (AU) ATURES LOCALION/Qualifiers 1. 11832	cgctgag 	ACACACACACACACACACACACACACACACACACACAC
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đ	16	CAGCCGAAGCTGGTCTGGTATGGGAGGCCGCCGTCCCGCGCGCG	820
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셤	5821	ccccaacacreccecrecarrererranaeaceceeeeceee	880
δ å	88	cccagctcgggcccggtgcggcgagctcaagcagttcctcg 5	
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. Оу	6061	gaggaggagagagagacccgggtgagcagcctccacaacacc 6	120
අ	6061	CGTGGGGGGTAAAGGAGCAGAGAAGAGAGAGACCCGGGTGAGCAGC	~
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ପୁ	6181	AGAGGTAAGGGGGTCTGGGTGTGGGGCCTACAGCAGTC	040
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М М Result

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A70382 Sequence 12
A70384 Sequence 14
A70388 Sequence 18
AF059293 Homo sapt
A70394 Sequence 24
A70393 Sequence 23
A70393 Sequence 23
A7005302 Mus muscu
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M80475 Mouse CCP5
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Nicola, N.A., Fabri, L., Farley, A., Nash, A., Willson, T., Rakar, S., Zhang, J., Alexander, W., Hilton, D.J., Kojima, T., Maeda, M. and Kikuchi, Y.
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AUTHORS
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                                                                              September 28, 1999, 16:40:47; Search time 3489.95 Seconds (without alignments) 6071.835 Million ceil updates/sec
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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.
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                                                         OM nucleic ; nucleic search, using sw model
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420 others
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                                                                                                                                                8427 g 10272 t
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8839 c 8427
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Source
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ORIGIN
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312 tttatgactgatgttttaaaaatttttatttgattttatgaaaatatacctgtttgtattt 371 1; Gaps Score 120.2; DB 34; Length 39061; Pred. No. 5.8e-19; 0; Mismatches 53; Indels 1; G Query Match
Best Local Similarity 75.1%;
Matches 163; Conservative

7672 Traaccacreaaniarcreaccaccerriririririririaagarririrgerri 7731

Search completed: September 28, 1999, 16:46:12 Job time: 7359 sec

gottoccaagtgottagattaaaggtgtgcactgcca 528

492

us-09-037-657-28.rng

Truncated upstream Upstream region of

1 V34386 1 V34385

89.6 89.6

444

ALIGNMENTS

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

September 28, 1999, 16:46:31; Search time 303.81 Seconds (without alignments) 5487.080 Million cell updates/sec

US-09-037-657-28 6663 Title: Perfect score: Sequence:

IDENTITY_NUC Scoring table: 311585 segs, 125096042 residues Searched:

N_Geneseq_36:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

,	Description			liced murine	haemopoleti	Novel haemopoietin	Togor	8	otide seq	cDNA encoding rat	encoding	encoding an	otide sequ	reoride sedn	roduct for h	1-alpha-OHa	1-alpha-OHa	v .	Boulus EPCR	ryropnil	ar endothel	sed sequenc	100	PlA genomi	A antiqen pre	genomic DNA	2 protein	2 protein gen	protein	2 protein gen	eotide se	equence encodi	ntlaily e	ednence encod	nce encodin	e creatin	ESX tran	Sequence encoding	otide seque	neutroph	ine GCSF re	nusculus	Mouse ST2L gene. A
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1381 ATCTGGTGTGT	1441 graagtggggc 	1501	1561 ccagca 1561 CCAGCA	1621 0	1681	1741 gagaca 1741 GAGACA	1801	1861 gaactcaaaag 	1921 agtacca 1921 AGTACCA	1981 cctatgaga 1981 CCTATGAGA	2041 cactgga 2041 CACTGGA	2101	2161 agccacggtg 	2221	2281 aacacctggc 	2341 ggactgagag 	Oy 2401 gggggggggggag Db 2401 GGGGGGGGGGGAA	Oy 2461 taattagggtgt
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Ωp	2581	GIGCCCCTGGCTCATTCCCACATCCAGAGTTTTGTGTTCTTCCTGGCATCTAACCCTCAG 2640	<u>අ</u>	3661
ΟŸ	2641	ttgtgctctgtggctggcaggctgcccgtggaggctcttggtaatgtacaaggcatca 2	δ	3721
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g	2761	GATATACAATAAAGCTT	අධ	3841
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qq	2821	TIGACATCACTCTC	음 	3901
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	δy	4621	tacttctacactgaaactgaactctcgcagacgcatatgctcactttaatgatgatgaa	1680
	qq	4621	CTTCTACACTGAACTGAACTCTCGCAGACGCATATGCTCACTTTAAT	0891

o do	4681	ataatggggaaactgaggttcgagagattctggaggaagaggtcaaaaccagctcca 4740 	Q .	
Qy Dp	4741	ggaagctctccagccccatccgggcctctccaggttctgggcttggcgggagtgaacac 4800 	ko da	5821 gececacacactgec
65 26	4801	agctgggaggggctggagctgggagctttggcccttgctcgtgcccagcacctgcgatt 4860 	AG G	5881 AGCCGCGGGGCGCGCGAG
oy og	4861	cttgcacgggagccagcaggcgctgcgtccgccgagagactgaagaagccgggggtag 4920 	. αα 	5941 gctggc
oy ob	4921	ggttggaggaggtaagcaggggctgtgggggccgaagcttgtgccagggcctgtcagcg 4980 	OY OY	6001 gtgcttggatgcagaagt
QY Ob	4981	agtccccagttttatttattggcgtgaggccgatgtccttatccgctggcctgctggggga 5040 	QQ QD	6061 gcgtggggggtaaagga
Oy Op	5041	tggctgcggctggggattggacccaagggctggcttcccactcagtcctccagcccactc 5100 	40 	6121 gcact 6121 GCACT
Qy	5101	catgicacaccogigcaticicigagotiatotigggaaccogcotigitotgigotg 1160	do do	6181
Qy Dp	5161	tetgtetetatttetgteatteaettteeaagageetttttttt	do do	6241 teetteggtgttgeteaagg 6241 TCCTTGGTGTTGCTCAAAGG
ογ	5221	tacgttttaaaaattgcttttgtataatgtgtgtgccttcgtgagcgtgcgt	da da	6301 aggttttactgcatc
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දු පු	5701 5701	1 tggcattgccattcctctgggtgactctgggtccacacctgacacctttcccaactttcc 5760	·	AC V27148; DT 29-SEP-1998 (first entry) DE Nucleotide sequence for mun KW Haemopolisin receptor; cell
84,	5761	1 ccagccgaagctggtctggtatgggaggccgccgtcccgcgcgcg	_	v ceil survival; cherapeutic; Wouse,

), nurine NR6 containing additional 5N sequence. Il proliferation; cell differentiation; cancer; c; neuronal proliferation; drug screening; ss; igetegggeeeggtgeggegegegeteaageagtteeteg 5940 tctctttagagcgccgggcccgggcggggggggggggtgtag 32 BP.

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Tor modulating proliferation, differentiation and survival of cells,

For modulating proliferation, differentiation and survival of cells,

Claim 9: 182pp; English.

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Cherapeutics used for modulating neuronal proliferation, differentiation

Cherapeutics used for modulating neuronal proliferation, differentiation

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Claim 9: 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; English 182pp; Engl
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                                                                           (AMRA-) AMRAD OPERATIONS PTY LTD.
(DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
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Best Local Similarity 99.6%; Pred. No. 0;
Matches 6628; Conservative 0; Mismatches
                                                              ÁU-002246.
                          19-MAR-1998.
11-SEP-1997; G02479.
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Mus sp.
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g	10222		
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γo	5232	cttogtgagcgtgccacaacacacacgtg	7
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δŏ	5352	tetegecagececteactteceatectgtttggata	
g	10522	GCAATTACTGAGTCATCTCGCCAGCCCCTCACCTCCATCCTTCCCATCCTTTGGATAG 1058	
δλ	41	gccta 5471	-
g G	10582	CATAGGIAATCGAAGGIAAATCGCTGGCTTTAATTTCGTAGCTATCCTGCCTCAGCCTA 1064	
Qγ	5472	caagtgctgtgctaccacgtttgtgggaggggctctcccagtgtctgggggggg	
g	10642	AAGIGCIGIGCIACCACGITIGIGGGAGGGCTCTCCCTCCCAGIGITGGGGGGT-ACA 1070	
ŏ	5532	cccttgctttgtccgtg 559	
<u>업</u>	10701	AGTCCCAAGATCTCTGCTTTCTAGGTCTTTGTCTTAGCTCTTGCCCCTTGTTTGT	
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δλ	5652	ccgtggcattgcc	7
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δ	5712	acctttcccaactttccccagccgaag	п
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oy.	5772	gtcccgcgcgcgcctcctgctggccgcgccccaacac	п
<u>점</u>	10941	361C16FAIGGAGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	8
δŏ	5832	tttagagcgcccgggcccgggcggcggcgtgtgcgagccgcggg	-
අ	11001	ccerrcearrererrandescececedececedecedecedecedecedecedeced	09
δ	5892	ggcgagcccagctcgggcccggtgcggcgcgagctcaagcagttcctcggctggct	-
셤	11061	DGAGCCCAGCTCGGGCCCGGTGCGCGCGCGCTCAGCAGTTCCTCGGCTGGCT	20
ογ	5952	tagtttccgcctgtacgaccagtggcgtgcttggat	п
g	11121	SCACGCATACTGCTCGAACCTTAGTTTCCGCCTGTACGACCAGTGGCGTGCTTGGATG 1118	80
å	6012	gaaaccaggtaggaaagttggggggaggcttgcgtggggg	-
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ογ	6072	gagacccgggtgagcatccacaacaccgcactcttc	
තු .	11241	GGAGCAGAGGAGAGAGACCCGGGTGAGCACCTCCACAACAACACCTCTTTT 1130	00

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NR6 is a novel haemopoictin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g., to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.
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                                                                                                                                                                                                               GGGTCTGGGTGAGTGGGGCCTACAGCAGTCTAGATGAGGCCCTTTCCCCTTCGGTGT 11420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unspliced murine NR6 nucleotide sequence.
Haemopoletin receptor; cell proliferation; cell differentiation; can
cell survival; therapeutic; neuronal proliferation; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated haemopoletin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells Example 8; Page 99-100; 182pp; English.
                                                                                                                                                                                                                                                                                                                                        aattggagcccctctgtaccatctgggcaacaaagaaacctaccagaggctgggcacaat
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tocaagcacaggacgagggatoctgcctcgggcagacggggtgcggcgagaggtaagg
               gggtctgggtgagtggggcctacagcagtctagatgaggcctttccctccttcggtgt
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(AMRA-) AMRAD OPERATIONS PTY LTD.
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Alexander W. Fabri L. Farley A, Hilton DJ, Kikuchi Y,
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
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11-SEP-1996; AU-0022
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WPI; 98-260970/23.
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WO9811225-A2.
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29-SEP-1998 (first entry)
Novel haemopoletin receptor; R6.3 gene.
Haemopoletin receptor; cell proliferation; cell differentiation; cancer; cell survival; therapeutic; neuronal proliferation; drug screening; ss; Mouse.

Mus sp. Location/Qualifiers
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Length
             Indels
Score 738.8; DB 1;
Pred. No. 1.3e-185;
); Mismatches 27;
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11.1%;
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Query Match
Best Local Similarity
Matches 778; Conserv
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Mus sp.
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The haemopoietin receptor (HR) NRG.3 is a form of the novel HR NRG.

The haemopoietin receptor (HR) NRG.3 is a form of the novel HR NRG.

Theraction between the novel HR and a ligand facilitates proliferation, differentiation and survival HR and a ligand facilitates proliferation, differentiation and survival maintenance or regeneration in an array of corresponding to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in the charapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, correction and diagnosi
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                                                                                                                                               11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS PTY LTD.
(DZIE) DZIEGLEWSKA H. ON
ALZARANGET W. FADTI L. Farley A, Hilton DJ, Klkuchi Y,
KOJima I, Maeda M, Nash A, Nicola NA, Rakar S, Willson
                                                       "Haemopoietin receptor NR6.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 738.8; DB 1;
Pred. No. 8.7e-186;
0; Mismatches 27;
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96.38;
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Best Local Similarity 96.3
Matches 778; Conservative
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P-PSDB; W55013.
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proliferation; cell differentiation; cancer;
neuronal proliferation; drug screening; ss;
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(DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
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Pred. No. 3e-64;
0; Mismatches 1;
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29-SEP-1998 (first entry)
Novel hemopoletin receptor NF
Haemopoletin receptor; cell pr
Cell survival; therapeutic; ne
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Best Local Similarity 99.6
Matches 281; Conservative
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11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
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us-09-037-657-28.rng

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V27143 standard; cDNA; 834 BP V27143;
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                                                    RESULT
V41688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   c.g. neuronal cells

Claim 5; Page 84-87; 182pp; English.

The haemopoletin receptor (HR) NR6.2 is a form of the novel HR NR6.

Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.

Sequence 1673 BP; 344 A; 550 C; 474 G; 335 T;
                                                                                                                                                                                      V27141;
29-SEP-1998 (first entry)
Novel hemopoietin receptor NR6.2 gene.
Haemopoietin receptor; cell proliferation; cell differentiation; cancer; cell survival; therapeutic; neuronal proliferation; drug screening; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ccctggctaaccttaatgggtccaggcagtcaggagacaatctggtgtgtcacgcc 1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1159 acacagotgtaatcagoccccaggaccccaccttctcatcggctcctccctgcaagcta 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                atggtcgcctgccttgcctgtgccgcctccttaacacctccaccctggcctgg 1338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 ACACAGCTGTAATCAGCCCCCAGGACCCCACCTTCTCATCGGCTCCTCCCTGCAAGCTA 308
                         368 ATGGTCGCCGCCTGCCCTCTGAGCTGTCCCGCCTCCTTAACACCTCCACCCTGGCCCTGG 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; W55012.
New isolated haemopoletin receptor - used for developing products
for modulating proliferation, differentiation and survival of cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          369 ATGGTCGCCGCCTGCCCTCTGAGCTGTCCCGCCTCCTTAACACCTCCACCTGGCCCTGG
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                                                                                                                                                                                                                                                                                                                                                                                        (AMRA-) AMRAD OPERATIONS PTY LTD.

(DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
KOJima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                             /product= "Haemopoietin receptor NR6.2"
                                                                              gagacggcagcattctggctggctcctgcctctatgttggct 1440
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                                                                                           488 GAGACGCAGCATTCTGGCTGGCTCCTGCCTCTATGTTGGCT 529
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Pred. No. 3.1e-64;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .1278
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Local Similarity 99.6%;
hes 281; Conservative (
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11-SEP-1996; AU-002246.
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DR WPI; 98-414109/35.

P. PSDB; W59804.

NPI; 98-414109/35.

P. PSDB; W59804.

NPI; 98-414109/35.

P. PSDB; W59804.

New nucleid acid encoding U4 haematopoietin receptor superfamily the nucleid acid encoding U4.

PT chain - potentially useful, e.g. for modulating cell proliferation or immune response, for treating cancer and auto:immune disease.

PT chain 1; Pages 25-26; SBPD; English.

This is the nuclectide sequence encoding the murine U4 protein from the haematopoietin receptor superfamily, used in the method of the immune case of the immune case of the immune case of the immune case of the immune case of the immune case of the immune case of the immune case of the immune case of the immune case of the immune case of the immune case of the immune case of the immune case of the immune case of the immune case of the immune case of the immune diseases, cancer, and allergy).

Sequence 1656 BP; 318 A; 552 C; 478 G; 308 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                               superfamily;
dy; cell differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1219 cctgctctatacatggagacacacctggggccaccgctgaggggctctactggaccttca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1279 atggtcgccgcctgccctctgagctgtcccgcctccttaacacctccaccctggccctgg
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Pred. No. 2.1e-63;
0; Mismatches 3;
                                                                                                                                       antibody;
                                                                                                                                                                                                                                                                                                                                                                                           15-JAN-1998; U00334.
16-JAN-1997; US-784863.
(GEMY ) GENETICS INST INC.
COLLINS M, DONALGSON DD, Neben T, Whitters M;
                                               7.26-007-1998 (first entry)
Nucleotide sequence of the murine U4 gene.
Murine: U4 protein: haematopoletin receptor
cell proliferation; immune response; antibod
autoimmune disease; cancer; allergy; ds.
                                                                                                                                                                                                                                                                                                              /product= "U4 protein"
                                                                                                                                                                                                                      Location/Qualifiers
122. 1399
/*tag= a
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Best Local Similarity 98.9%;
Matches 279; Conservative (
V41688 standard; cDNA; 1656
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RESULT 10
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Claim 7; Page 93-95; 182pp; English.

The nucleotide sequence was generated by a 5N RACE of brain cDNA using NR6 specific primers. NR6 is a novel Haemopoletin receptor (HR).

Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.

Sequence 834 BP; 167 A; 274 C; 225 G; 168 T;
29-SEP-1998 (first entry)
Nucleotide sequence of products generated by 5N race of brain cDNA.
Haemopoletin receptor; cell proliferation; cell differentiation; cancer; cell survival; therapeutic; neuronal proliferation; drug screening; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1245 ggggccaccgctgaggggctctactggaccttcaatggtcgccgcctgccctctgagctg 1304
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CDNA encoding rat Zcytor5
Zcytor5: cytokinin-like receptor; down-regulation; growth factor;
maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
cardiac pathology; heart enlargement; Zcytor5 ligand; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated haemopoietin receptor - used for developing products for modulating proliferation, differentiation and survival of cells.
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                                                                                                                                                                                                                                                                                                                                         (AMRA-) AMRAD OPERATIONS PTY LTD.
(DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Koʻlima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
                                                                                                                                                                                                                         "Haemopoletin receptor
                                                                                                                                                   Location/Qualifiers
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Matches 255; Conservative
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                                                                                                                                                                                                                                                                                               11-SEP-1997; G02479
                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang J;
WPI; 98-260970/23.
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V70896
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The present sequence encodes a protein designated Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-requiate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletel muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the therapeutically to andidy 2cytor5 ligand effects.

Sequence 1724 BP; 350 A; 550 C; 500 G; 324 T;
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17-MAR-1999 (first entry)
CDNA encoding human zcytor5.
CSYtor5; cytokinin-like receptor; down-regulation; growth factor;
maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
cardiac pathology; heart enlargement; Zcytor5 ligand; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
down-regulating Zcytor5 natural ligands or detecting cardiotrophin-1
in blood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1724;
                                                                                                                                                                                                                   01-MAY-1997; US-045287.

01-MAY-1997; US-850030.

13-FEB-1998; US-0218890.

(ZYMO) ZYMOGENETICS INC.

Adams RL, Foster DC, Glibert T, Jelmberg AC, Lehner JM, Lok S, Presnell SR, Whitmore TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.7%; Score 248; DB 1;
92.9%; Pred. No. 1.2e-55;
ative 0; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 72-75; 55pp; English
Location/Qualifiers
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                                                     /*tag= a //product= Zcytor5
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Best Local Similarity 92.9
Matches 260; Conservative
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P-PSDB; W70862.
                                                                                                                                                             01-MAY-1998;
13-FEB-1998;
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Provent to blood

PS Disclosure; Page 68-70; 55pp; English.

Disclosure; Page 68-70; 55pp; English.

Disclosure; Page 68-70; 55pp; English.

CC Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be daministered to down-regulate the effects of a growth and/or maintenance of actor in thyroid, heart, and skeletal muscle for example to lessen the ceffect of cardiotrophin-1 on cardiac pathologies, so preventing heart calculargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence cand integrity of the Zcytor5 gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcytor5 and the count indiotypic antibody 2cytor5 ligand effects.

CC therapeutically to modify Zcytor5 ligand effects.

So Sequence 1813 BP; 415 A; 604 C; 519 G; 275 T;
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Nucleotide sequence of the human U4 gene.
Human; U4 protein; haematopoietin receptor superfamily;
cell proliferation; immune response; antibody; cell differentiation;
autoimmune disease; cancer; allergy; ds.
                                                                                                                                                                                                                                                                                            New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g. down-regulating Zcytor5 natural ligands or detecting cardiotrophin-1
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                                                                                                                                                                    Jelmberg AC, Lehner JM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1399 gagacggcagcattctggctggctcctgcctctatgttggc 1439
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86.8%; Pred. No. 1.1e-48;
iive 0; Mismatches 37
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15-JAN-1998; U00334.
16-JAN-1997; US-784863.
(GENY_).GENETICS INST INC.
CCOllins M, Donaldson DD, Neben T, Whitters in WPI; 98-414109/35.
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1. 1228
/*tag= a
/product= "U4 protein"
13-FEB-1998; US-074721.

01-MAY-1997; US-045287.

01-MAY-1997; US-850030.

13-FEB-1998; US-023890.

(ZYMO ) ZYMOGENETICS INC.

Adams RL, Foster DC, Gilbert T, Je

Lock S, Presnell SR, Whitmore TE;

WPI; 99-034662/03.
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V41689;
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Matches 244; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure: Page 63-66; 55pp; English.

The present sequence encodes a protein designated Zcytor5, which is a cytokinin-like receptor: Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-l on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-l in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcytor5 and therapeutically to modify Zcytor5 ligand effects.

Sequence 1690 BP; 319 A; 592 C; 505 G; 274 T;
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CDNA encoding an allelic varaint of human Zcytor5.

Zcytor5: cytokinin-like receptor; down-regulation; growth factor;

maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
cardiac pathology; heart enlargement; Zcytor5 ligand; allelic varaint;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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86.8%; Pred. No. 1e-48;
tive 0; Mismatches 37; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37; Indels
                                                                                                                                                                                                                                                                 Jelmberg AC, Lehner JM,
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88. .1365
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                                                                                                                                                                                                                  (27MD) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert T,
Lok S, Presnell SR, Whitmore TE;
P-PSDB; W70860.
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V70895;
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                                                        01-MAY-1998; U08865.
13 FEB-1998; US-074721.
01-MAY-1997; US-045287.
01-MAY-1997; US-850030.
13-FEB-1998; US-023890.
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01-MAY-1998; U08865
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Query Match

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in blood

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Gaps

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Length 1813;

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Human.
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               New nucleic acid encoding U4 haematopoietin receptor superfamily chain - potentially useful, e.g. for modulating cell proliferation or immune response, for treating cancer and auto:immune disease claim 1, Page 28; 38pp; English.

This is the nucleotide sequence encoding the human U4 protein from the haematopoietin receptor superfamily, used in the method of the invention for the modulation of cell proliferation or the immune crosponse. Transformed mammalian cells are used to produce recombinant U4 protein is used to stream for specific binding as tissue markers for isolation of cognate ligands and receptors, and in pharmaceutical compositions which may modulate cell proliferation, cell differentiation, and the immune system (e.g. for treating immune deficiency, inherited or the result of infection, autoimmune diseases, connect, and allery).
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Nucleotide sequence of clone HFK-66 encoding human NR6.
Haemopoietin receptor; cell proliferation; cell differentiation; cancer; cell survival; therapeutic; neuronal proliferation; drug screening; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1219 cctgctctatacatggagacacacctggggccaccgctgaggggctctactggaccttca 1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coctggctaaccttaatgggtccaggcagtcaggagacaatctggtgtgtcacgccc 1398
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11-SEP-1997; GD2479.
11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS PTY LTD.
(DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
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86.5%; Pred. No. 2.6e-48;
11ve 0; Mismatches 38;
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n 7; Page 102-104; 182pp; English.
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Best Local Similarity 86.5
Matches 243; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9811225-A2
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e.g. n
Claim
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The NR6 gene encodes a novel Haemopoietin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening. Sequence 1391 BP; 281 A; 459 C; 417 G; 234 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haemopoletin receptor; cell proliferation; cell differentiation; cancer cell survival; therapeutic; neuronal proliferation; drug screening; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3434 gigaccacggacccccacccgacgigacgigagccgcgtiggggcctgggacgaggaccag 3493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3494 etgagtgtgggtctcaccaccagctctcaaggatttcctctccaagccaagtac 3553 | 1111 | 1111 | 1111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3614 egeceetgaeceegeeecegeatetgaetecteecteacegtgeaggtggtggtggaeg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 1391;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37;
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Best Local Similarity 73.5%; Pred. No. 1.5e-40;
Matches 291; Conservative 0; Mismatches 37
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29-SEP-1998 (first entry)
PCR product for human NR6.
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WPI; 98-260970/23
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WO9811225-A2.
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Disclosure; Page 111; 182pp; English.

NR6 is a novel haemopoletin receptor (HR). Interaction between the novel
HR and a ligand facilitates proliferation, differentiation and survival
of a wide variety of cells. The HR and it's derivatives can be used for
modulating the activity of the receptors e.g. to regulate development,

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New polynucleotides encoding 25-hydroxyvitamin D 1-^a-hydroxylase -
useful to detect and treat vitamin D-related disorders
Example 4, Page 79-81; 85pp; English.

This invention describes novel 25-hydroxyvitamin D 1-alpha-hydroxylase
(1-alpha-OHase), a renal cytochrome P450 enzyme of the vitamin D
pathway, and polynucleotides encoding the enzyme from human, mouse and
rat tissue. Molecules of the invention are used to diagnose and treat
vitamin D-related disorders, to produce vitamin D metabolites, and to
identify modulators of the enzyme expression. The invention describes
an animal cell transformed with the enzyme promoter which is used to
identify compounds which modulate activity of the polynucleotide
encoding the enzyme, and to modulate the production of vitamin D in
patients with vitamin D endocrine disorders in the vitamin D in
patients with vitamin D to alapha 25(0H)2D3.

25-hydroxyvitamin D to 1 alpha 25(0H)2D3.

Sequence 4105 BP; 1063 A; 1032 C; 1063 G; 947 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
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maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for
                               vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.

Sequence 560 BP; 113 A; 182 C; 165 G; 100 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                             3520 GITITITGGITITCCCAGACAGGGITICICIGIGIAACCCIGGCIGITC-TGGAACTCAC 3462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3580 TITACCITITATCIATITGTATTTTAGAGICACIGIGGGGITTTTTTGTTTGTTTGTTTT 3521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3494 ctgagtgtgcgctgggtctcaccaccagctctcaaggatttcctcttccaagccaagtac 3553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse 1-alpha-OHase promoter region DNA #2.
1-alpha-OHase; vitamin D 1-alpha-hydroxylase; vitamin D pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            renal cytochrome P450 enzyme; 25-hydroxyvitamin D; human; mouse;
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Pred. No. 1.8e-18;
0; Mismatches 51; Indels 1;
                                                                                                                                                                                                                                                                                                 Length 560;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis; treatment; disorder; endocrine; promoter; ss
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                                                                                                                                                                                                                                                                                             Score 141.2; DB 1;
Pred. No. 1.2e-27;
0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHRINERS HOSPITALS FOR CHILDREN
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Matches 150; Conservating
                                                                                                                                                                                                                                                                                                 2.1%;
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                                                                                                                                                                                                                                                                                                                        Best Local Similarity 92.0
Matches 149; Conservative
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06-AUG-1997; US-906791.
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Best Local 3
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1 (bases 1 to 447)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Email: Robert_Strausbergenih.gov
This clone is available royalty-free through LLNL ; contact the
TMSC Consortium (info@image.llnl.gov) for further information.
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                             1159 acacagotgtaatcagcccccaggaccccaccttctcatcggctcctccctgcaagcta 1218
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                                                                                                                                                                                                            Score 220.2; DB 43; Length 477;
Pred. No. 6.2e-44;
0; Mismatches 38; Indels 0;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebra
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Unpublished (1997)
On Aug 21, 1998 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert Length: 1667 Std Error: 0.00 Seg primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 431.
Location/Qualifiers
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                                                                                                                                                                                                            3.3%;
Similarity 86.5%;
13; Conservative
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Matches 243;
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AI187074
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AI269388 417 bp mRNA EST 27-JAN-1999
q126b05.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1857585
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 417)
NCI-CGAP http://www.ncbi.nlm.nih.gov/nclcgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Tel: (301), 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                            Length 447;
                                                                                                                                                                                                                                                                    1 others
                                                                                                                                                                                                                                                                                                                                    Score 220.2; DB 43; Length
Pred. No. 6e-44;
0; Mismatches 38; Indels
/clone_11D="Soares_fetal_lung_NbHL19W"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
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175 c 128 q
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3.3%;
Best Local Similarity 86.5%;
Matches 243; Conservative (
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Unpublished (1997)
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FEATURES

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/lab_host="Delta" Life Technologies)"
/lab_host="Public Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polyllnker; Site_1: Not I; Site_2: Eco RI: The UI-R-G0
library is a normalized library constructed from a
mixture of rat tissues (nodose ganglia, dorsal root
ganglia, and trigeminal ganglia). The tag is a string of
6 nucleotides present between the Not I site and the
oligo-dr track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6:
791-806, 1996."
  451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Tel: 319 335 9565
Email: 319 335 9565
Email: msoares@blue.weeg.ulowa.edu
Oligo-dr track not found, Not I site shown in beginning of sequenc is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
Seq primer: M13 Forward.
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Eutheria; Primates; Catarrhini; Hominidae; Ho
ICI (Dases 1 to 41)
NCI -CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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Pred. No. 7.6e-44;
O; Mismatches 19;
                                                                                                                                                                                                                                                                                                      /clone="UI-R-G0-ut-h-08-0-UI"
/clone_lib="UI-R-G0"
                                                                                                                                                                                                                                         /organism="Rattus norvegicus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69
t
                                                                                                                                                                                                                                                          /strain="Sprague-Dawley/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                 /dev_stage="adult"
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Best Local Similarity 92.4%;
Matches 231; Conservative (
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AI333812
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Ratus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Wurinae; Rattus.
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 332)
Bonaldo,M.F. Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                            /clone="rwAGE: 857585"
/clone_lib="Soares_NhHMPU_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
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CDNA clone
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86.5%; Pred. No. 5.9e-44;
Atlive 0; Mismatches 38; Indels 0;
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UI-R-GO-ut-h-08-0-UI.s3 UI-R-GO Rattus norvegicus
UI-R-GO-ut-h-08-0-UI 3', mRNA sequence.
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97044477
                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
ity sequence stop: 406.
Location/Qualifiers
                                                                                                                                                                  pregnant uterus" /lab_host-"DH108"
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AI579568.1
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Length 332; Indels 1278

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13-FEB-1999

VERSION , KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL MEDLINE COMMENT

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RESULT AIS79568

ACCESSION

us-09-037-657-28.rst

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                                                                                                                                                                                                                                                                                                                                                                                                                          double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot - 5. Library constructed by Bento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 constructed by Bento
1brary was constructed
                                                                                                                                                                                                                                                                                                                                                             National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                           This clone is available royalty free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1615 Std Error: 0.00 Seg primer: -400P from Gibco High quality sequence stop: 407.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soares and M.Fatima Bonaldo. This library was construct
from the same fetus as the fetal heart library, Soares
fetal heart NDHH19W."
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Unpublished (1997)
On Jan 14, 1998 this sequence version replaced g1:1797892.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 3.3%; Score 219.2; DB 45; Length Similarity 86.4%; Pred. No. 1.1e-43; 12; Conservative 0; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                             /clone_lib="Soares_fetal_lung_NbHijgw"
/dev_stage="19 weeks"
/lab_host="bHi0B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1400 agacggcagcattctggctggctcctgcctctatgttggc 1439
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                                                                             Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                              'organism="Homo sapiens"
'db_xref="taxon:9606"
                                                                                                                                                                                                                                                                             /map="4p16.1-4pter"
/clone="IMAGE:1930606"
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A1670108.1
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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. " 156 c 108 g 66 t
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/clone=lib="Soares_thymus_NHFTh"
/dev_stage="fetal"=thymus_NHFTh"
/lab_host="Diga" (phage-resistant)"
/note="Organ: thymus_pooled; Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 385) NCI-CGAP http://www.ncbl.nlm.nlh.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@inh.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 372.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 ACGGCGCCCCCCTGAGCTCTCCCGTGTACTCAACGCCTCCACCTTGGCTCTGG
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Unpublished (1997)
On May 9, 1996 this sequence version replaced gi:1133091
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1larity 85.4%; Pred. No. 8.8e-43;
Conservative 0; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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1 (bases 1 to 482)

1 (bases 1 to 482)

1 (bases 1, to 482)

2 (barra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T 3'), on equal amounts of mRNA from 2 13.56pc and 2
14.56pc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M. Ertima Bonal And
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                     Waterstön,R.
The WashU-HHMJ Mouse EST Project
Unpublished (1996)
On Apr 14, 1993 this sequence version replaced g1:785250.
                                                                                                                                                                                                                                                                                                                                      Washu-HHMI Mouse EST Project
Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louls, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGI:239573
Possible reversed clone: similarity on wrong strand
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.2%; Score 214.8; DB 26; Similarity 81.1%; Pred. No. 1.3e-42; 5; Conservative 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 359.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C57BL/6J"
/db_xref="taxon:10090"
/map="10 pter-cen"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: ETPrimer
  W66776.1 GI:1375694
                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                             Mus musculus
                                           house mouse.
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Thermostabilization and thermoactivation of thermolabile enzymes by Thermostabilization and thermoactivation of the synthesis of full length cDNA trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))

Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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On Jun 22, 1998 this sequence version replaced gi:3246782.
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Wus musculus adult C57BL/6J cerebellum Mus musculus cDNA
clone 1500034F20, mRNA sequence.
AV032198
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                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 262)
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                                                        -----AGGTGGTGGATGAC
                                                                                                                       gtcagcaaccagacctcctgcogtctcgcgggcctgaagcccggcaccgtttacttcgtc
cegeceetgaececegececeegcatetgaetecteceteaecegtgeaggtggtggatgae
                                                                                                                                                                                      145 GTCAGCAACCAGACCTCCTGCCGTCTCGCGGGCCTGAAGCCCGGCACCGTTTACTTCGTC
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Tel: 81-298-36-9145
Fax: 81-298-36-9098
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/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
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/clone="1500034F20"
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Genome Science Laboratory
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by Bonaldo, Lenno
791-806, 1996."
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Best Local Similarity 92.0
Matches 218; Conservative
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JOURNAL
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AUTHORS
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Fax: 319 335 9565
Email: msoares@blue.weg.uiowa.edu
011go-dr track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
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//dab_host="DH10B [Life Technologies]"
/note="Vector: pT73D-Pec (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-G0
library is a normalized library constructed from a
mixture of rat tissues (nodose ganglia, dorsal root
ganglia, and trigeminal ganglia). The tag is a string
6 nucleotides present between the Not I site and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                              6423 gotcacetgaattggageeeetetgtaeeatetggggeaacaaagaaacetaeeagagget 6482
                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                            AI574687 319 bp mRNA EST . 30-MAR-1999
UI-R-GO-uc-b-11-0-UI.S1 UI-R-GO Rattus norvegicus CDNA clone
UI-R-GO-uc-b-11-0-UI 3', mRNA sequence.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On May 18, 1998 this sequence version replaced
   Pred. No. 3e-42;
); Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
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/clone_lib="UI-R-G0"
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Seq primer: M13 Forward.
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                                                                                                                                                                                                                                                                                                                                  242 AAAGGAGTTGTTCAGGTCCCG 262
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   93.58;
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Best Local Similarity 93.5
Matches 244; Conservative
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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Genome Research 6:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 390)
Marra,M., Hilliar,L., Allen,M., Bowles,M., Districh,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Thelsing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                             1159 acacagotgtaatcagococoaggaccocacottotcatoggotoctcoctgcaagota 1218
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                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W17583 390 bp mRNA EST 10-SEP-1996 mb75b01.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:335209 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_11D="Soares mouse p3NMr19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: p1773D (Pharmacia) with a modified
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                                                                                                                                                                     Length 319;
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                                                                        1 others
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This clone is available royalty-free through LLNL
IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                  19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis,
Fax: 314 286 1800
                                                                                                                                                                        DB 48;
ck. The library was Lennon and Soares, G
                                                                                                                                                                   Score 207.2; DB 48
Pred. No. 8.7e-41;
0; Mismatches 19,
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Location/Qualifiers
1. 390
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1st strand cDNA
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                      6425 tcacctgaattggagcccctctgtaccatctgggcaacaaagaaacctaccagaggct-g 6483
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                                                                                                                                                                                                                                 6365 aggtoctgccggctaaactctaaggataggccatcctcctgctgggtcagacctggaggc 6424
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                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                           Query Match
3.0%; Score 200.2; DB 26; Length 390;
Best Local Similarity 97.4%; Pred. No. 5.1e-39;
Matches 225; Conservative 0; Mismatches 3; Indels 3;
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Search completed: September 28, 1999, 15:38:38 Job time: 3306 sec

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mi99d07.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:474733 5', mRNA sequence. A039053 91514788
                                                                                                                               Score
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AA039053/c
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DEFINITION
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                                                             3; Search time 2095.87 Seconds (without alignments) 6270.900 Million cell updates/sec
                                                                                                    GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
                                                                                                                                                                    2546578 segs, 986266752 residues
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                                      nucleic search, using sw model
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em_est3:
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Perfect score:
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AV032198 AV032198
AI574687 UI-R-GO-U
MI7581 MD75501.1
AA04291 ZK5661.8
RR7407 YM88409.81
AA04228 UI-K-AO-B
AA049278 UI-R-AO-B
AA049278 UI-R-AI-E
AA042592 UI-R-AI-E
AA925924 UI-R-AI-E
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AI670108 we65f03.x
W66776 me17b11.rl
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Match Length
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ALIGNMENTS

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Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases I to 445)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelseb,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T 3'), on equal amounts of mRNA from 2 i3.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated t
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo.
129 c 124 g 107 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205 TCACCTGAATTGGAGCCCCTCTGTACCATCTGGGCAACAAGAAACCTACCAGAGGCTGG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   jh LLNL ; contact the
further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 AGTCCTGCCGGCTAAACTCTAAGGATAGGCCATCCTCCTGCTGGGTCAGACCTGGAGGC 206
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                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        embryo NbME13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 248; DB 27; Length 445; Pred. No. 8.1e-51; 0; Mismatches 0; Indels ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'tissue_type="embryo"
'dev_stage="13.5-14.5dpc total fetus"
'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free through
IMAGE Consortium (info@image.llnl.gov) for fu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 441.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . .445
organism="Mus musculus"
                                                                                                                                                                                                                                                                     The WashU-HHMI Mouse EST Project Unpublished (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="IMAGE:474733"
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Best Local Similarity 99.6
Matches 259; Conservative
                                                  Mus musculus
                                                                                                                                                                                                                                           Waterston, R.
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T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo." 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                        AI394468 462 bp mRNA EST 30-MAR-1999
tf79d12.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2105495 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bonaido, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Cente:
Clone distribution: NCI-CGAP clone distribution information can |
Cound through the I.M.A.G.E. Consortium/LLNL at:

www-bio.lnl.gov/bbrp/image.html
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                                                                                                                                                                                                                                                                                                                                          Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 46.2)
NCI/NINDS-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)
On Feb 17, 1998 this sequence version replaced gi:2887603.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 ACACAGCIGIGATCAGTCCCCAGGATCCCACGCTTCTCATCGGCTCCTCCTGCTGGCGCCA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
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/clone_ilb="MCI_CGAP_Brn23"
/tissue_type="911oblastoma (pooled)"
/lab_host="DH108"
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Pred. No. 2.5e-44;
0; Mismatches 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insert Length: 1631 Std Error:
Seq primer: -400P from Gibco
High quallity sequence stop: 454.
Location/Qualifiers
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/map="10; 1"
6604 aggagttgttcaggtcccga 6623
                                                                                                                                                                                                                                                                          AI394468.1 GI:4224015
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86.8%;
                                         AGGAGTTGTTCAGGTCCCGA
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AI394468
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Best Local Simi
Matches 244;
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Gaps

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1339

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1399

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/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: heart; Vector: pT73D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Ist strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTACCAAGTGGAAGGGGCCCATCTTTTTTTTTTTTTT 3'), double-stranded cDNA was size selected, ligated to Eco RI addapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="839C02: 821G11; 4; 4p15.33-4p16.1; 4p15.33-4p16.1"
/clone="IMAGE:1705398"
                                                                                                                                            acacagetgtaateageeeceaggaceecaceetteteateggeteeteetgeaageta 1218
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Butherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 10466)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                              1219 cctgotctatacatggagacacactggggccaccgctgaggggctctactggaccttca 1278
                                                                                                                                                                                                                                                                                                                                                                                                         1339 ccctggctaaccttaatgggtccaggcagtcaggagagacaatctggtgtgtcacgccc 1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1599 Std Error: 0.00
                                                                                                                                                                   AI161002 466 bp mRNA EST 26-OCT-1998 qb69g04.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705398 3', mRNA sequence.
                                                                                                                                                                                                                                                            On Jan 19, 1998 this sequence version replaced gi:2287379.
                                                                 Length
                                                                                                          Indels
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/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1399 gagacggcagcattctggctggctcctgcctctatgttggc 1439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 GIGACGCCAGCATCCTGGCTGGCTCCTGCCTCTATGTTGGC 334
                                                           Score 221.8; DB 46;
Pred. No. 2.5e-44;
0; Mismatches 37;
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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AI161002.1 GI:3694307
                                                        Query Match 3.3%;
Best Local Similarity 86.8%;
Matches 244; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A1421423 474 bp mRNA EST 30-MAR-1999 tf25h01.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2097265 3's similar to SW:IL6B_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN A1421423
                                                                 coctggctaacottaatgggtccaggcagcagtcaggagacaatctggtgtgtcacgccc 1398
1 (bases 1 to 474)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BFGAP), Tumor Gene Index
Unpublished (1998)
on Apr 7, 1998 this sequence version replaced gi:3034955.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IxMAE:3097265"
/clone_lib="NCI_CGAP_Brn23"
/tlssue_type="qlioblastoma (pooled)"
/lab_host="DH108"
                                                                                                                                                                                                                                       www-bio.llnl.gov/bbrp/image/image.html
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Seq primer: -400P from Gibco
High quality sequence stop: 450.
Location/Qualifiers
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81

BASE COUNT ORIGIN

source

FEATURES

AI421423.1 GI:4267354

Homo sapiens

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

VERSION KEYWORDS SOURCE ORGANISM

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 466)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/nclogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert-Strausberg@inh.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1622 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 466.
                                                                                                                                                                                                               acacagotgtaatcagccccaggaccccaccttctcatcggctcctccctgcaagcta 1218
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qe44h04.xl Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
IMAGE:1741879 3', mRNA sequence.
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Unpublished (1997)
On Jan 19, 1998 this sequence version replaced g1:2151491.
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/organism="Homo sapiens"
/db_xref="taxon:9006"
/clone="IMAGE:1741879"
/clone_lib="Soares_fetal_lung_NbHL19W"
/dev_stage="19 weeks"
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Pred. No. 6.1e-44;
0; Mismatches 38;
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AI185780.1 GI:3736418
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Best Local Similarity 86.5%;
Matches 243; Conservative
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double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI185924 477 bp mRNA EST 29-OCT-1998 qe50c05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1742408 3' similar to TR:Q16354 Q16354 PROLACTIN RECEPTOR ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncb1.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 477)

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Unpublished (1997)
On Feb 17, 1998 this sequence version replaced gi:2150926.
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Pred. No. 6.1e-44;
0; Mismatches 38; Indels
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/dev_stage="19 weeks"
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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/clone="IMAGE:1742408"
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Matches 243; Conservative
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AI185924
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Title: Perfect score:

Run on:

Sequence:

Scoring table:

Database :

Searched:

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222412 H.saplens 2
222412 H.saplens 9
AL008583 Human DNA
294778 H.saplens 9
22459 F.fluoresce
AL031317 Streptomy
D86087 Human DNA
AL031429 Human DNA
AL031429 Human DNA
AC07226 Home sapl
AC07226 Home sapl
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AC05028 Home sapl
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Y07848 Homo saplen

AC000026 Homo sapl

M7745 R. norvegicu

AL049886 Homo sapl

AE014348 Rhodococc

U44891 Rhodococcus

AL031035 Streptomy

M64859 S. lividans

AF127374 Streptomy

AF031612 Oryctolag
Y07919 M.musculus
AC005528 Mus muscu
AL049478 Mycobacte
L78823 Mycobacteri
D30760 Streptomyce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unclassified.

1 (bases 1 to 35)
Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S., Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and Kikuchi,Y.
A NOVEL HARMOPDIFIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME Patent: WO 9811225-A 19-MAR-1998;
NICOLA NICOS ANTONY (AU)
Location/Qualifiers
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Sequence 30 from Patent WO9811225.
A70400
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HS327J16
HSDNASTAO
PFPQQABCF
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AC006014
RHMHSNAD
RMNODEFG
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AC005098
AC005488
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                                                                                 September 28, 1999, 16:46:12; Search time 3489.95 Seconds (without alignments) 31.895 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
        GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
                                                                                                                                    US-09-037-657-30
35
1 agctggcgcgcccccgggcggatcgggagcccac 35
                                                                                                                                                                                                                     679419 seqs, 1590154680 residues
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                                                         OM nucleic - nucleic search, using sw model
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07-MAY-1999

Score 35

Result No.

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Gaps

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RESULT 2 MMBPRADPR/c

Matches

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ORGANISM

VERSION KEYWORDS SOURCE

REFERENCE

AUTHORS

TITLE

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Direct submission

Submitted (25-M06-1998) Department of Chemistry And Blochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
Ok 73019, USA
On May 29, 1999 this sequence version replaced g1:4510435.

* NOTE: This is a "working draft" sequence. It currently
* consists of 7 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be preserved
* by the finished sequence as soon as it is available and
the accession number will be preserved
* by the finished sequence as soon as it is available and
the accession number will be preserved
* 2246: contig of 2246 bp in length
* 5237 6162: contig of 17789 bp in length
* 6233 24021: contig of 17789 bp in length
* 64426 73433: contig of 2638 bp in length
* 46426 73433: contig of 26938 bp in length
* 73503: gap of unknown length
* 73503: gap of unknown length
* 73504: Gap of unknown length
* 73507: Gap of unknown length
                                                                                                                                                                                                                                                                                       ACOO5528 195923 bp DNA HTG 29-MAX-1999
Mus müsculus, WORKING DRAFT. SEQUENCE, 7 ordered pleces.
ACOO5528
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 195923)
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        Length 3885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fang, F., Ying, F., Pan, H., Dumanski, J. and Roe, B.A. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fang, F., Ying, F., Pan, H., Dumanski, J. and Roe, B.A.
Mus musculus PAC Clone 493n6 In MDR Region
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        Score 22.2; DB 12;
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Pred. No. 69;
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/db_xref="taxon:10090"
50392 a 48306 c 47825 g 48972
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HTG; HTGS_PHASE2.
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        Query Match 63.4%;
Best Local Similarity 77.1%;
Matches 27; Conservative (
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ORIGIN
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (11-SEP-1996) C. Guilbaud, Dept. Of Molecular Medicine, Clinical Genetics Unit, Karolinska Hospital, Building L-6, S-171 76 Stockholm, SWEDEN
                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Characterization of a mouse homologue for human beta-prime-adaptin
gene; CDNA sequence, genomic structure and chromosomal localization
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SISHDLQLINKALQVATDFAIQFNRNSFGLAPAAPLQVHVPLSPNQTVEISLPLNTVG
SVLKMEPLNNLQVAVKNNIDVFYFSTLYPLHVLFVEDGKADRQMFLATWKDIANENEA
OFQIRDCPLNTEAASNKLQSSNIFTVAKRNVEGQDMLYQSLKLTNGIWVLAELRIQPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OIFILDCLDNYMPRDDREAGSICERVTPRLSHANSAVVLSAVKVLMKFMEMLSKDLDY
YATLLKKLAPPLVTLLSAEPELQYVALRNINLIVQKRPEILKHEMKVFFVKYNDPIYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klekldimirlasqaniaqvlaelkeyatevdydfyrkavraigrcaikveqsaercy
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LATQDSDNPDLRDRGYIYWRLLSTDPVAAKEVVLAEKPLISEETDLIEPTLLDELLCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3885) Gullbaud,C., Fransson,I., Clifton,S.W., Roe,B.A., Carter,N. and Dumanski,J.P.
                                                               Gaps
                                                                                                                                                                                                                                                                                                              10-SEP-1997
                                                               ö
        Length 35;
                                                            0; Indels
                                                                                                                                                                                                                                                                                          MMBPRADPR 3885 bp mRNA ROD.
M.musculus mRNA for beta-prime-adaptin protein.
Y07919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product="beta-prime-adaptin protein"
  ch 100.0%; Score 35; DB 5; Stailarity 100.0%; Pred. No. 0.082; 35; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome="11"
clone_lib="whole mouse embryo"
clone_lib="mouse brain"
                                                                                                                1 agctggcgcctcccgggcggatcgggagcccac 35
                                                                                                                                                   1 AGCTGGCGCCCTCCCGGGCGGATCGGGAGCCCAC 35
                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'db_xref-"MGD:MGI:1096368"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             orotein_id="CAA69224.1"
|b_xref="PID:e266088"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .ocation/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                      X07919.1 GI:2398719
beta-prime-adaptin protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="351"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 3885)
Suilbaud, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1050 c
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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source

FEATURES

TITLE JOURNAL

REFERENCE AUTHORS

JOURNAL

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Gaps

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BASE COUNT

ORIGIN •

RESULT MLCL458

SOURCE

us-09-037-657-30.rge

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/clone="cosmid L458"
                          misc_feature
                                                                                             gene
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                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eiglmeier,K., Honore,N., Woods,S.A., Caudron,B. and Cole,S.T.
Use of an ordered cosmid library to deduce the genomic organization
of Mycobacterium leprae
Mol. Microbiol. 7 (2), 197-206 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    are also included but some to the codes is given for each CDS.

In codoss is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. All CDS over 100 codons have been analysed. Gene prediction is based on positional base preference in codons especially where there is an increase in the observed/expected third position G + C. CAUTION:
                                                                                                                                                                ALO49478.1 GI:4539121
chaps, CoA.apo-[Acyl Carrier Protein]; DNA polymerase III alpha
chaln; dnaE; fas; ilva; isoleucyl-FRNA synthetase;
L-asparaginase; L-glutaminase; lipoprotein signal peptidase; lspa;
oxidoreductase; pseudogene; pseudouridine synthase; RLEP element;
rluC; threonine dehydratase biosynthetic; type I fatty acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Work in Paris is supported by the Heiser Trust, the Association Francaise Raoul Follereau and the Groupement de Recherches et des Etudes des Genomes (GIP-GREG).
Details of M. leprae sequencing at the Sanger Centre are available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the World Wide Web.

RL, http://www.sanger.ac.uk/Projects/)
S are numbered using the following system eg MLCB33.01c. ML (M. prae), cB33 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the Sanger Centre is funded to complete the sequence of M. leprae by the Heiser Program for Research in Leprosy and Tuberculosis of the New York Community Trust.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (15-MAR-1998) Mycobacterium leprae sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge Banger E-mail: barrellesanger.ac.uk Cosmids supplied by Dr. Stewart T. Cole, [3] Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 tue du Docteur Roux, 75724 Paris Cedex 15, France Requests for cosmids should be sent to Karin Eiglmeier
                                                  24-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence MAY NOT be the entire insert of the clone. It may be shorter because we only sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 (bases 1 to 43839)
James, K.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      small overlap between neighbouring submissions.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5-13bp before the initiation codon). If this we choose the most upstream initiation codon.
                                                  BCI
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                       миссь458 43839 bp DNA
Mycobacterium leprae cosmid L458.
AL049478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 43839)
eeger, K.J. and Harris, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 43839)
                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium leprae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fycobacterium.
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                                                                                                                                                                                                                                                                                                                                                                             synthase
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AUTHORS
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TITLE
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KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
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COMMENT

/db_xref="taxon:1769"

FEATURES

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/translation="MQSLRRHFTCRSTFYHGYISLPAQRAVVRTSTADTHLDSTMTGA
AGENQRYTNQHPAVDQVGRLSGSVTVTPAPRSVGRTVSPADDLLDDSFCHSGTNPFLD
QVAVFPSADLKPQLRNTAKFRAVDHGHEVQPWLDFVAMVIPP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'translation="Mleknrpoifdsfdrilkarspeawlsrrkeidlhstifeytlk'
JABERRRNPSDDIWRTLASAVITGNDEKPFRLPANELEFFFVLTFTGSNTAKHTTGYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation-"MQLAPEWRQGGEPVFIIAVKVYTILLSGHIQNGRTSSHRIEYSL
FLYNHRHLCLSSSEDGQVGGKSDDEPTRREPVSRQRNTGRSELPF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown function, N-terminus similar to internal sequence of YP22_MYCTU (EMBL:280226) Rv0778 (MTCY369.22) M. tuberculosis hypothetical protein (414 aa), fasta scores; opt: 192 z-score: 189.2 E(): 0.0031, 31.4% identity in 102 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MLCB458.03c, hypothetical protein, len: 89 aa;
unknown function, improbable CDS based on frame analysis"
                                                                                                                                                                                                                                                                  aa;
'note-"overlap with cosmid B1701 from 19932 to 20500"
                                                                                                                                           complement(97. .531)
/gene="MLCB485.01c"
/note="MLCB485.01c"
/note
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="MLCB458.02c, hypothetical protein, len: 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="hypothetical protein MLCB485.01c"
protein_id="CAB39566.1"
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protein_id="CAB39567:1"
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/product-"hypothetical protein MICB458.03c"
/protein_id="CAB39568.1"
/db_xref-"PID:e419861"
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note="MLCB458.04c, hypothetical
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/gene="MLCB458.03c"
/note="MLCB458.03c, hypo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref-"PID:e1419859"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'db_xref-"PID:94539122"
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fnote="MTCB458.02c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'db_xref-"GI:4539122"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein id-"CAB39569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="PID:q453912
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                                                                        gene="MLCB485.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     label-MLCB485.01c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label-MLCB458.02c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="MLCB458.02c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label-MLCB458.04c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'codon_start=1
                                                   complement (97
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6

gene

SGS

/codon_start=1 /transl_table=11

.14186

gene

CDS

/gene="fas" 4956. .1418 1926.

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Eiglmeier, K., Honore, N., Woods, S.A., Caudron, B. and Cole, S.T. Use of an ordered cosmid library to deduce the genomic organization of Mycobacterium leprae Mol. Microbiol. 7 (2), 197-206 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone. Coding sequences larger than 60 amino acids were predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_lib="Lorist 6"
/note="The liver of the armadillo was used to isolate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 An attempt was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MA, 02154. Please contact Doug Smith further information. The sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was generated by the Genome Sequencing Center at Genome Therapeutics Corporation (Collaborative Research Division),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the presence of a Shine-Dalgarno sequence, or overlapping orf tha suggested translational coupling. It is possible that the actual
                                                                                                                                                                                                                                                                                                                                                                                                                  Smith, D.R., Richterich, P., Rubenfield, M., Butler, C., Lee, H.-M., Swith, D.R., Richterich, P., Rubenfield, M., Butler, C., Lee, H.-M., K. V.O., Gunderson, K., Chung, M., Maher, J.K., Deloughery, C., Aldrich, T. Imitch, J., Tulig, C., Smyth, A., Drill, S., Avruch, A.S., Rice, P., Abendschan, K., Aldredge, T., DeLoughery, C., Kirst, S., Safer, H., Connelly, S., McDougall, S., Eiglmeier, K., Bergh, S., Cole, S., Robison, K., Jaehn, L., Gryan, G., Church, G.M. and Mao, J. Prepublication submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILP 2188 bp DNA BCT 07-FEB-1999 Streptomyces erythraeus gene for trypsin-like protease, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence may not represent the entire cloned insert of
                           Mycobacterium leprae (clone: cosmid B13) (tissue library: Lorist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         insert of a Lorist 6 cosmid clone from a mapped set of clones constructed from M. Leprae genomic DNA isolated from armadillo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to locate the most probable start site based on codon usage,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
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                                                                                                Mycobacterium leprae
Bacteria; Firmlcutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                          Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the basis of codon usage and homology information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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/db_xref="taxon:1769"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.3%; Score 21.8; DB 1;
llarity 78.8%; Pred. No. 1.4e+02;
Conservative 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .42923 /organism-"Mycobacterium leprae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 17290 GCTGGCGCCCACCCCGGCACATCGCAAGTCCA 17258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8223 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             site differs from the one selected. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 gctggcgcgctcccgggcggatcgggagcca 34
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13528 c 11679 g 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beaver St., Waltham, (smith@cric,com) for
                                                                                                                                                                                                       Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 26; Conserv
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                                                                                                   ORGANISM
                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
STMTLP/c
                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (27.1% identity in 1739 as overlap). C-terminus similar to N terminus of TR:069474 (EMBL:AL023635) MLCB1243.20c, kasA, M.Eprae beta-ketoacyl-ACP synthase (414 as) (27.5% identity in 386 as overlap) and TR:069473 (EMBL:AL025635) MLCB1243.19c, kasB, M.leprae beta-ketoacyl-ACP synthase (425 as) (25.1% identity in 382 as overlap). Equivalent to TR:P95029 (EMBL:AL98363) Rv2524c (MTCY159.32-MTV090.09c) M.tuberculosis FAS (3069 as) (85.8% identity in 3081 as overlap). Contains Pfam match to entry PF00698 and overlap). Contains Pfam match to entry PF00698 Acyl_transf, Acyl transferase domain. score 18.20, E-value 1.98-08, PS00017 Athyer-binding site motif A (P-loop) and PS00606 Beta-ketoacyl synthases active site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MLCB458.06, fas, probable type I fatty acid
synthase, len: 3076 aa; similar to many eubacterial and
sukaryotic FAS e.g. TR:059497 (EMBL:X87822) Brevibacterium
ammoniagenes FAS (3063 aa), fasta scores; opt: 5361
z-score: 5527.0 E(): 0, 44.3% identity in 3106 aa overlap.
N-terminus shows similarity to FASI_CANAL (EMBL:X74952)
candida albicans FAS beta subunit (2037 aa) (27.3%
identity in 1928 aa overlap) and C-terminus to FAS2_CANAL
(EMBL:L29063) Candida albicans FAS alpha subunit (1885 aa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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KGNTADWLGGATAGLRHAQRGYQLHTAAGGPVSAPIYASIDSNPTYEQYKQQVAPYLR
SWESVIGHQRTGVYANSRTIAWALQDGLASYFWQHNWGSPKGYTHPAANLHQVEIDRR
   /translation="MTERMTAWYRIPGKIAAREIPATALVNSVNPKIPLWPAESYRRM
RCDTTSYRVDSFDSDFVIDSHQSLSIVAVERSAQIAKQLAISGCS"
                                                                                                                                         3625. .4344

Agone="MLCB458.05"

Anote="MLCB458.05"

Anote="MLCB458.05"

John Third TR:P95028 (EMBL:283863)

RV5525c (MTCY159.31) M.tuberculosis hypothetical protein

RV5225c (MTCY159.31) M.tuberculosis hypothetical protein

RV5225c (ATCY159.31) M.tuberculosis hypothetical protein

RV5225c (ATCY159.31) M.tuberculosis hypothetical protein

RV5225c (ATCY159.31) M.tuberculosis hypothetical protein

RV525c (ATCY159.31) M.tuberculosis hypothetical protein

RV526 M.T. (ATCY159.31) M.tuberculosis possible

N-terminal signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MSVSRRDVLKFATVTPGLLGLGVAAAALCAVPASTAGSLGTLLD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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/protein_id="CAB39571.1"
/db_xref="PID:e1419864"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 43839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="hypothetical protein MLCB458.05"
/protein_id="CAB39570.1"
/db_xref="PID:e1419863"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 21.8; DB 1; Length 4
Pred. No. 1.3e+02;
0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSGB13GS 42923 bp DNA BCT Mycobacterium leprae cosmid B13 DNA sequence. L78823
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table-11

Query Match Best Local Similarity 78.8%; Matches 26; Conservative

GI:1377768

g1377768 L78823.1

NID VERSION

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LOCUS DEFINITION MSGB13GS/c

RESULT

ACCESSION

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NID VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

JOURNAL REFERENCE AUTHORS TITLE

JOURNAL MEDLINE

COMMENT

REFERENCE AUTHORS

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Direct Submission
Submitted (01-APR-1993) Zabarovsky E., Karolinska Institute, Tumor
Biology, S-104 01 Stockholm, Sweden
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted (03-MAY-1995) Zabarovsky E.R., Microbiology and Tumorbiology Center, Karolinska Institute, P.O. Box 280, Stockholm, S-171 77, SWEDEN
                                 1 (bases 1 to 239)
Sabarovsky.E., Kashuba,V., Pettersson,B., Petrov,N., Zakharyev,V.,
Gizatullin,R., Lebedeva,T., Bannikov,V., Erlandsson,R., Uhlen,M.,
Kisselev,L. and Klein,G.
                                                                                                       Shot-gun sequencing strategy for long range genome mapping: first results
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo saplens"
/db_xref="taxon:9606"
/chromosome="3 (human)"
/cell_line="mouse/human microcell hybrid line MHC 903.1"
/clone_lib="NotI linking library"
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalla; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
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Eukaryota, Metazoa, Chordata, Vertebrata, Mammalia, Eutheria,
Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 239)
Zabarovsky,E.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSNL2273D 239 bp DNA PRI 01
H.sapiens genomic DNA (chromosome 3; clone NL2273D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 21.4; DB 10;
Pred. No. 6.8e+02;
0; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                             chromosome="chromosome 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                            26
                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggcgcgccccggggggatcgggagcccac 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACGAGCCTCCCGGGCGGCTGGGGAGTCCCC 56
                                                                                                                                                                                                                                                                                                                                                                                  /clone="NL22273D"
/cell_line="MCH903.1"
/clone_lib="NL2"
75 c 52 g
                                                                                                                                                                                                                                                                                                                                                                                                                                        52 g
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Submitted (03-MAY-1995)
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80.6%;
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llarity 80.6%;
Conservative
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Zabarovsky, E.R.
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Best Local Similarity
Matches 25; Conserva
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                                                                                                                                                    Unpublished
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Best Local 9
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HSNL2273D/c
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ACCESSION
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SOURCE
ORGANISM
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ORIGIN
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AUTHORS
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MSSNEGTVSKVTNVWVHPEYQDAAKGFDVSVLTLEAPVKEAPIELAKADDAGYAPDTA
ATILGWGNTSEGGQQADHLQKATVPVNSDDTCKQAYGEYTPDAMVCAGVPEGGVDTCQ
                                                                                                                                                                                                                                                                                                                         3 (bases 1 to 2188)
Nagamine-Natsuka, Y., Norioka, S. and Sakiyama, F.
Molecular cloning, nucleotide sequence, and expression of the gene encoding a trypsin-like protease from Streptomyces erythraeus
J. Blochem. 118 (2), 338-346 (1995)
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                                                                                                                                                                                              Submitted (18-MAY-1994) to the DDBJ/EMBL/GenBank databases. Sh Norloka, University of Osaka, Institute for protein research; /amadaoka, Suita, Osaka 565, Japan (Tel:06-879-8618, aax:06-876-2533)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                         Saccharopolyspora erythraea
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Pseudonocardineae; Pseudonocardiaceae;
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/Organism="Saccharopolyspora erythraea"
/db_xref="taxon:1836"
1049. :1867
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/product="trypsin-like protease"
/protein_id="BAA66423.1"
/db_xref="PID:dl006993"
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Pred. No. 3.8e+02;
0; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (18-May-1994) to DDBJ by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              509 GGAGGGCACCGGACGGAGGGGGGGGCGCAC 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Institute for protein research
University of Osaka
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                   trypsin-like protease.
Streptomyces erythraeus DNA
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H.sapiens DNA sequence.
222412
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80.6%;
                                                                                                                       Saccharopolyspora.
I. (bases 1 to 2188)
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06-876-2533.
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                                                                                                                                                                              Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shigemi Norioka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamadaoka
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Matches 25; Conserva
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Homo sapiens
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Z22412.1
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source

CDS

FEATURES

Query Match

BASE COUNT ORIGIN

LOCUS DEFINITION ACCESSION

VERSION KEYWORDS SOURCE ORGANISM

RESULT 7 HSDNASGAT/C

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Gaps

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Indels

Length 239;

Gaps ö Length 239; 'note="genomic DNA surrounding NotI sites'
75 c 52 g 56 t 2 others Indels Score 21.4; DB 10; Pred. No. 6.8e+02; 0; Mismatches 6;

LOCUS

HS327J16/c

RESULT

ò 셤 ORGANISM

SOURCE

KEYWORDS

VERSION

ACCESSION

REFERENCE AUTHORS

JOURNAL

COMMENT

FEATURES

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/note="match: cDNA AB010031; match: ESTS AA829582 AA675540
AA270574 AI12243 AA560435 AA007825 AA796378 AA681606.
AA320574 AI12243 AA560435 AA007825 AA796378 AA681606.
AA322556 H55197 AA340185 AA895042 AA431647 AA278275
AA0399563 N42713 AA076578 T48120 W01618 AI182462 AI084123
AA039955 AA403935 AA935522 AA431283 AA076579 AA435541
AA625556 AA4427946 AI208576 AI222283 AA176559 AA73557
AA52555 AA4207946 AI208576 AI22283 AI146563 AA725572
AA56555 D60397 D60888 D60658 AA431647 D81455 D80477"
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Fsunnesaakmiketmdkkfgssmhuvigegfgfeithevknllylyfggtlaucum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="dJ327J16.1 (human ortholog of mouse outer arm
Dynein light chain 4)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(6902. .7066,8379. .8462,10116. .10184))
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                                                                                                                                                                                                                                                     3819. 3897

/note="L2 repeat: matches 2447. .2528 of consensus"

4507. .4583

5473. .5697

/note="L2 repeat: matches 2486. .2709 of consensus"

/note="L2 repeat: matches 2486. .2709 of consensus"

21521. .21608))
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'note="L2 repeat: matches 2677. .2707 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .2698 of consensus"
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14570. .14681
                                                                  .2709 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MIR repeat: matches 22. .241 of consensus"
7980, .8010
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/note="MIR repeat: matches 4. .210 of consensus"
11960. 12265
                                                                                                                   repeat: matches 90. .144 of consensus"
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14682. .14993
                                                                                                                                                                                                                       repeat: matches 3. .181 of consensus"
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/note="L2 repeat: matches 1478.
11159. .11292
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//note="MIR repeat: matches 111.
11253. .11298
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1654. .11835
                                                                                                                                               240. .2347
note="MIR repeat: matches 123.
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                                                                  L2 repeat: matches 2615.
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product="dJ327J16.1 (human
yynein light chain 4)"
protein_id="CAA15429.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
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/gene="dJ327J16.1"
/note="match: STS G14738"
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                      copies 4 mer
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/note="MIR re
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                                            428
             note-"21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        requests: clonerequest@sanger.ac.uk
On Jan 16, 1999 this sequence version replaced gi:3892846.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the true left end of clone 150C2 (ALO22318) is at 111647 in this sequence. The true right end of clone 779B17 (ALO21806) is at 50467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMPORTANT: This sequence is not the entire insert of clone 327J16. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                        ALO08583.1 GI:4160195
HTG; CHROMODOX; CpG 1sland; Neuronal Pentraxin Receptor; outer arm
Dynein light chain 4.
                                                                                                                                                                                                              HS327J16 111746 bp DNA PRI 15-JAN-1999 Human DNA sequence from clone 327J16 on chromosome 22ql2.3-13.2. Contains three novel genes: the human ortholog of mouse outer arm Dynein light chain 4, the human ortholog of rat Neuronal Pentraxin Receptor and a novel member of of the CHROMODOX protein genes family. Contains ESTs, STSs, a GSS and putative CpG islands,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          327216 is from the library RPCI3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpcc.med.buffalo.edu/ VECIOR: pCTPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (28-DEC-1998) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 111746)
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/note="129 copies 2 mer ca 58% conserved"
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/note="71 copies 4 mer tcca 82%
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/note="AluSx repeat: matches 1. 875. 1158
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ote="Tigger3b repeat: matches 992. .1231 of consensus"
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Ote="L2 repeat: matches 2289, .2620 of consensus"
484. 17605
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                                                                                                      .2747 of consensus"
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19. .23559
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                                                                                                 note="L2 repeat: matches 2678. .2747 of consensus 5513. 16720
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 .313 of consensus
                                    .149 of consensus
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te-"match: CpG 1sland clones 279875 279876"
60. .21158
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'note="AluSg repeat: matches 2.
14994. 15027
note="MIR repeat: matches 116.
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6498. .16566
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ö 2 (bases 1 to 348)
Zabarcvsky, E.
Direct Submission
Submitsted (01-APR-1993) Zabarovsky E., Karolinska Institute, Tumor
Biology, S-104 01 Stockholm, Sweden
Location/Qualifiers Gizatullin, R.Z., Kashuba, V.I., Protopopov, A.I. and Zabarovsky, E.R. Zabarovsky, E., Kashuba, V., Pettersson, B., Petrov, N., Zakharyev, V., Gizatullin, R., Lebedeva, T., Bannikov, V., Erlandsson, R., Uhlen, M., Kisselev, L. and Klein, G.
Shot-gun sequencing strategy for long range genome mapping: first Submitted (18 APR-1997) Zabarovsky E.R., Karolinska Institute, Microbiology and Tumorbiology Center, P.O. Box 280, Stockholm, S-171 77, Sweden Gaps 02-DEC-1997 Homo sapiens Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 315) 01-JAN-1995 Sūkaryota; Metazoa; Chordata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. /lab_host="mouse/human microcell hybrid MCH903.1" ö Length 315; Indels 1S294778 315 bp DNA PRI (clone NLIA177R). /note="sequence surrounding NotI site" 106 c 127 g 36 t 'clone_lib="NL1 Not! linking library PRI Query Match 60.6%; Score 21.2; DB 10; Best Local Similarity 76.5%; Pred. No. 7.3e+02; Matches 26; Conservative 0; Mismatches 8; 133 GCAGCCGCGACCCCCGGGGCGCTCCGGAGCCCAC 166 2 gotggogoctocogggoggatogggagcocac 35 /chromosome="chromosome 3"/germline .315
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Db 71360 GCGCCGCGCCTGCGGGGCCTCGGGCGCCCCC 71327

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Gaps ö Indels. Query Match 60.6%; Score 21.2; DB 9; Best Local Similarity 76.5%; Pred. No. 1.6e+02; Matches 26; Conservative 0; Mismatches 8;

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GFLICYDIEFPENARRIALAGAELILVPTANMIPYDFVADVTIRARAFENGCYVAYAN
YCGHERQIRYCGQSSIRAPDGSRIALAGLDEALIIGTLDRQLMGESRALNRYLSDRRP
ELYDDLSKR
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YAHFWQDDWFAEQRGIFIAGDDVSWTPAWVEGAVQTSLNAVWGIMKHFGGATHAENPG
DVFHEIGPIALAD"
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Submitted (18-MAY-1995) U. Schnider, Laboratoire de Biologie
MICROBIENTE, Batiment de BIOLOGIE, UNIVERSITE DE LAUSANNE, CH- 1015
Lausanne-Dorigny, SWITZERLAND
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schider, U., Keel, C., Voisard, C., Defago, G. and Haas, D.
Tn5-directed cloning of pqq genes from Pseudomonas fluorescens
CHAO: mutational inactivation of the genes results in
overproduction of the antibiotic pyoluteorin
Appl. Environ. Microbiol. 61 (11), 3856-3864 (1995)
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        19-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pqqA gene; pqqB gene; pqqC gene; pqqF gene; pyrroloquinoline quinone blosynthesis.
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                                                                                                                                                          Length 348
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/strain="CHAO"
                                                                                                                                                                                                                                                                                                                                                                   FFEQUABOR 5137 bp DNA BC1
P. fluorescens paqf, paqA, paqB, paqC genes.
X87299
99229799
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/db_xref="PID:9929800"
/db_xref="GI:929800"
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/db_xref="PID:g929801"
/db_xref="G1:929801"
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                                                                                                                                                       Score 21;
Pred. No. 8
                                                                                                                                                                                                                                                   ggcgcctcccgggcggatcgggagcccac 35
                                                                                                                                                                                                                                                                          113 GGGGGCCTGCTGGGGGGGGGGGGGCGCCAC 83
                       /cell_line="MCH903.1"
/clone_lib="NLM"
137 c 155 g
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/clone="NLMP238D'
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                                                                                                                                                     Ouery Match 60.0%;
Best Local Similarity 77.4%;
Matches 24; Conservative (
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Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces coelicolor sequencing at The Sanger Centre is funded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            available on the World Wide Web. (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c, SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Redenbach, M., Kieser, H.M., Denapaite, D., Elchner, A., Cullum, J., Kinashi, H. and Hopwood, D.A. A set of ordered cosmids and a detailed genetic and physical map for the B Mb Streptcomyces coelicolor A3(2) chromosome Mos. Microbiol. 21 (1), 77-96 (1996)
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Direct Submission
Submitted (19-AuG-1998) Streptomyces coelicolor sequencing proj
Sanger Centre, Wellome Trust Genome Campus, Hinxton, Cambridge
CB10 ISA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof.
David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
Colney, Norwich, Norfolk NR4 70H, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 5.4e+02;
0; Mismatches 9;
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                                   /db_xref="PID:9929806"
/db_xref="GI:929806"
/db_xref="SWISS-PROT:P55173"
/translation="MTDTPLSAAEF"
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Streptomyces coelicolor cosmid 6G4
protein_id="CAA60734.1"
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Best Local Similarity
Matches 26; Conserv
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97000351
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ACCESSION
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KEYWORDS
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correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream librosome binding site sequence (optimally 5.13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon. If the sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid 664 lies between D31 and D63 in the AseI-D genomic restriction fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation = "IAGRRVCRNEPKHVFHVTYTPPKKEGVCDVCGGELYQRDDDSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRCO adenylate kinase (EC
The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene
                                                                          prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the Frameplot program of Bibb et al., Gene 30:157-66(1984) as implemented at Littp://www.nih.go.jp/
Jun/cgi-bhi/Frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     994 aa; almost identical to KAD STRCO adenylate kinase (E 2.7.4.3) (205 aa) and highly similar to many e.g. KAD_SORDE adenylate kinase (EC 2.7.4.3)(218 aa), fasta scores; opt: 22 -score 429.1 E(): 1.2e-16, 50.6% identity in 85 aa overlap. Contains Pfam match to entry PF00406 adenylatekinase, Adenylate kinases, score 136.80,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              methionine aminopeptidase, len: 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adenylate kinase, partial CDS, len:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as; identical to TR:05408 (EMB::X83011) methionine aminopeptidase (278 aa) and highly similar to many e.g.AMPM_BACSU methionine aminopeptidase (EC 3.4.11.18 (248 aa), fasta scores; opt: 546 z-score: 912.2 E(): (44.5% identity in 256 aa overlap. Also similar to scorelicolor map2 (E(): 3.2e-33, 46.8% identity in 250 coelicolor map2 (E(): 3.2e-33, 46.8% identity in 250 overlap). Contains PS00680 Methionine aminopetidase subfamily 1 signature and Pfam match to entry PP00557
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s-value 1.4e-54"
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'note="possible RBS upstream of map"
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db_xref="SPTREMBL:086771"
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/note="SC664.02, map,
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/product="methionine aminopeptidase"

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1736. .1813

misc_feature

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1489. .1506
/standard_name="prostaglandin E receptor EP3 subtype gene"
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Submitted (19-JUN-1996) to the DDBJ/EMBL/GenBank databases. Masato
Kotani, Kyoto University Graduate School of Medicine, Dept. of Med.
and Clin. Sci: 54 Shogoin-kawahara-cho, Kyoto, Kyoto 606, Japan
(Tel:075-751-4285, Fax:075-771-9452)
2 (bases 1 to 1506)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kotani,M., Tanaka,I., Ogawa,Y., Usui,T., Nakao,K. and Narumiya,S.
The human prostaglandin E receptor EP3 subtype gene
Unpublished (1996)
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Kotani,M., Tanaka,I., Ogawa,Y., Usul,T., Tamura,N., Mori,K.,
Narumiya,S., Yoshimi,T. and Nakao,K.
Structural organization of the human prostaglandin EP3 receptor
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Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1506)
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Human DNA for prostaglandin E receptor EP3 subtype, exon 1
D86087
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80.0%; Pred. No. 8.5e+02;
11ve 0; Mismatches 6;
                    Score 20.4; DB 1;
Pred. No. 3.6e+02;
0; Mismatches 6;
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prostaglandin E receptor EP3 subtype.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Genomics 40 (3), 425-434 (1997)
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/clone_11b="lEMBL3"
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/gene="EP3-III"
361. :1488
/gene="EP3-III"
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                      58.3%;
80.0%;
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Matches 24; Conservative
                                                                 Conservative
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KPGGGKYGIIEDYGGHGIGTEMHMDPHLLNYVDRRRGKGPKLVPGFCLAIEPMVSLGT
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                                                                                        /translation="MVQIKNPEQIAKMREAGLVVAAIHAATREAAVPGATTKDLDQVA
RKVLAEHDAKPNFLGYGGFPATICTSVNEVVVHGIPSDDVVLKDGDVISIDGGAIIDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Pfam match to entry PF00444 L36, Ribosomal protein 136, score 70.40, E-value 3.1e-22" 1819
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/gene="infA"
/note="Pfam match to entry PF00575 S1, S1 RNA binding
motif, score 54.10, E-value 3.1e-12"
                                                                                                                                                                                                                                                                                                                                954. .1010
/gene-"map"
/note-"PS00680 Methionine aminopeptidase subfamily 1
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                                                                                                                                                                                                                     444. .1196
/gene="map"
/note="Pfam match to entry PF00557 pep_M24,
metallopeptidase family M24, score 194.80, E-value
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product="translational initiation factor IF1"
protein_id="CAA20381.1"
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'note="possible RBS upstream of rpmJ"
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note="possible RBS upstream of infA"
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/product="50s ribosomal protein L36"
/protein_id="CAA20382.1"
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/db_xref="SPTREMBL:054208"
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/db_xref="GI:3449238"
/db_xref="PID:e1316448"
/db_xref="PID:93449236"
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gene="infA"
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/qene="rpmJ'
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954. 10
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                                                                                                                                                                                                                                                                                                                                                                                              During sequence assembly data is compared from overlapping clones. Merca differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the corresponding to the overlapping clone name. Note that the corresponding to the overlapping clone, as we submit sequences submission or responding to the overlapping clone, as we submit sequences with The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Em:, EMBL; Sw., SWISSPROT; Tr:, TREMBL
This sequence is the entire insert of clone 333A15. This sequence
has been finished according to sequence map criteria as follows. An
attempt is made to resolve all sequencing problems, such as
compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was generated from part of bacterial clone contigs of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.sanger.ac.uk/HGP/cnr.
333A15 is from the library RPC13 constructed at the Roswell Park
Cancer Institute by the group of Pieter de Jong. For further
details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human chromosome 1, constructed by the Sanger Centre Chromosome Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /21. .1979
hote="LlME3A repeat: matches 5600. .5863 of consensus
                       133221 bp DNA PRI 12-MAY-1999 Sequence from clone 333A15 on chromosome 1p31.1-31.3
                                                                                                                                                                                                                                                                                                                                  Submitted (12-MAY-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1083. 1237
note="MER41B repeat: matches 481, .635 of consensus"
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Prinates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 133221)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note-"MER41-internal repeat: matches 2645. .3727 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .4653 of consensus"
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note="AluSx repeat: matches 1. .267 of consensus"
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'note="AluJb repeat: matches 1. .303 of consensus'
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/note="8 copies 4 mer acac 94% conserved"
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note="48 copies 2 mer at 83% conserved"
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/db_xref="taxon:9606"
/chromosome="1"
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                                                                                                                                   AL031429.11 GI:4775605
HTG; CpG Island.
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/note="L1P re
                                                                     complete sequence.
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note="HERVFH21 repeat: matches 9. .99 of consensus"
1372. .21487
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2653. .22796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIR repeat: matches 34. .192 of consensus." .31661.
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0989
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copies 4 mer tata 80% conserved'
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                                                                              185. 8759
note-"THE1A-internal repeat: matches 1.
                                                                                                                                                                                                                                                                                     .2710 of
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                                  conserved"
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                                                                                                                             8760. 9114
/note="http://www.natches 1.
9153. 9223
/note="12 repeat: matches 2424.
                                                                                                                                                                                                                                                                                                                                                                     2473. .12626
note≈"MER5A repeat: matches 6.
                                                              note="THELA repeat: matches 1.
                                                                                                                                                                                                                                                                                   repeat: matches 2550.
                                                                                                                                                                                                                                                                                                                                                                                                                       copies 4 mer ttaa 77%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ote="THEIA repeat: matches 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6793. .17146
note="THE1A repeat: matches 1.
7835. .18314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 repeat: matches 2245.
19353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat: matches 1948.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="MIR repeat: matches 12. 3312. .23485
                               ta 82%
                                                                                                                                                                                                                                                                                                      17 copies 2 mer at 918 .12034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat: matches 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="MIR repeat: matches 6. 1536. .23893
                               19 copies 2 mer
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                                                                                                                                                                                                                                                                /note-"L2 re-
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                                                                                                                                                                                                                                                                                                      .1999. .12
'note="17
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repeat: matches 5534. .6123 of consensus"
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                                                                                                                         repeat: matches 4491. .6300 of consensus"
                                                                                                                                                                                                      "Limae repeat: matches 4456. .4491 of consensus"
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                                                                                                                                                                   :e="AluSg1 repeat: matches 1. .295 of consensus"
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                                                                "AluSx repeat: matches 7. .284 of consensus" .35690
                                                                                                                                                                                                                                                     IC repeat: matches 1. .465 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                        1B repeat: matches 1. .364 of consensus"
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repeat: matches 11. .213 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                repeat: matches 3. .196 of consensus"
                                       copies 4 mer agga 73% conserved"
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49603
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Best Local Similarity 80.0%;
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Search completed: September 28, 1999, 16:46:27 Job time: 7374 sec

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(without alignments)
4003.939 Million cell updates/sec
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Sequence 5, Appl.
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                                                                                        September 28, 1999, 16:40:56; Search time 152.56 Seconds
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                                                                                                                                                                                                                                                                             Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/5C_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/5D_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS9_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS9_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
                                                                                                                                                                                                                                                176461 segs, 45838279 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                           OM nucleic - nucleic search, using sw model
                                                                                                                                                      US-09-037-657-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length DB
                                                                                                                                                                                                                  IDENTITY_NUC
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Score Match
                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                                                                  Scoring table:
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No.
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Appl Appl Appli Appli Appli Appli Appli Appli		.s. 1; 23 598 83
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Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence		1; tgta TGTA tccg
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	भूद ७	ULE TYPE: genomic DNA 0438-5 tch al Similarity 80.6%; Pred. No. 2.7e-17; al9; Conservative 0; Mismatches 30; Indels 1; G ttgtatttggtttggtttggtttggttttgtttatttgagacaggcttctctgtgtag
	no t Precurs Uses The	.; L 30; 30; 1111 1111 1111 1111
187-453-35 135-513-35 187-453-35 93-03993-1 93-03993-2 299-8498-5 232-463-14	s Beno igen P and Us the St.	DB 1 .7e-1 es tttga ttttga TTCGA
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US-08-187 US-08-135 US-08-187 PCT-US93- PCT-US93- US-08-299 US-08-299		Score 1 Pred. N ; Mism agttttg TTTTTTG
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10614 10614 10614 10614 5030 5032 4698 4698 7218		ULE TYPE: genomic DNA 0438-5 tch al Similarity 80.6%; p 119; Conservative 0; ttgtatttggtttggtttgattil
	"我们是一个一个一个一个一个一个一个一个一个一个一个一个一个一个一个一个一个一个一个	geno ty erva tttgg TTTT
00000000	TT 1 T = 00 - 0438 - 5 Tuent No. 5342774 ENERAL INFORMATION: Tuent No. 5342774 ENERAL INFORMATION: Tuent OF INVENTION: f Application Of Section Of The Of Section Of Section Of The Of Section Of Section Of Section Of Section Of The Of Section Of The Of Section Of The Of Section Of The Of Section Of The Of Section Of Section Of The Of Section Of The Of Section Of The Of Section Of The Of Section Of The Of Section Of The Of Section Of The Of Section Of The Of Section Of The Of Section Of The Of Section Of The Of Section Of The Of Section Of The Of Section Of The Of Section Of The Of Section Of The Of Section Of The Of The Of Section Of The Of The Of Section Of The Of T	LE TYPE: ge 438-5 1 Similarity 1 Similarity 1 Lili
	1043B-5 107-043B-5 10.07-043B-5 10.05 Applica 10.05 Applica 10.05 INVENTI MEDICANT 10.05 INVENTI MEDICAL 10.05 APPLICATIO 10.05 APPLICATION 10.05 APPLICATIO	TYPE: -5 -5 -5 -7 -1111 TITIT
557.8 556.8 551.4 550.8 6.08	1 107-0438-5 ince 5, 4pp PLIAL INFORM TIE NO 5342 TIE OF INV THE OF INV STATE: NO STATE: NO STATE: NO STATE: NO STATE: NO STATE: NO TIE OF INV TIE OF INV TIE OF INV TIE OF INV TIE OF INV THE O	COLE : -043B each cal S 129 ttgtz ttgtz TTTT ttcctc
	T 1 -807-043 -807-043 -807-043 -807-043 -807-04 -807-0	
88444444 800112840	SULT 1 Squence 5, Applicate Patent No. 5342714 GENERAL INFORMATION APPLICANT: BOOD. TITLE OF INVENTIC NUMBER OF INVENTIC NUMBER OF SEQUENCE OF THE STREET: New YOTE STREET: NEW FILING DATE: 2 PRIOR APPLICATION NUM FILING DATE: 2 PRIOR APPLICATION NUM FILING DATE: 3 PRIOR APPLICATION NUM FILING DATE: 2 PRIOR APPLICATION NUM FILING DATE: 3 ATTORNEY ABOUT STREET	MOLECULE S-07-807-043 Query Match Best Local Matches 12 364 ttg 1539 TTT
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1539 TITITITITITITITITITITITITITITITITITICAGACAGGGTTTCTCTTIGIAT 1598
                                                                                                             1599 CCCTGGCTGTCC-TGGCACTCACTCTGTAGACCAGGCTGGCCTCAAACTCAGAAATCTGC 1657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 99; DB 1; Length 135
Pred. No. 2.3e-17;
0; Mismatches 35; Indels
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                                                                                                                                                                                 /PE: Floppy disk
: IBM PC compatible
s Fystem: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                        484 ctgcttgtgcttcccaagtgcttagattaaaggtgtgcac 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CUCREDIT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,390
FTI.ING DATE: 19910910
                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/07757390 Patent No. 5453491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Pennie & Edmonds
1155 Avenue of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,87.
REFERENCE/DOCKET NUMBER: 7,
TELECOMMUNICATION INFORMATION
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Takagi, Satoshi
APPLICANT: Murata, Yoshiyuk:
TITLE OF INVENTION: Human An
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 8698864/9741
5141 PENNIE
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Best Local Similarity 78.4%;
Matches 131; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
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US-07-757-390-4
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APPLICANT: De Plaen, Etlenne; Boon-Falleur, Thierry;
APPLICANT: Leth , Bernard; Szikora, Jean-Pierre; De Smet, Charles;
APPLICANT: Chomez, Patrick
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful in
TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor
1599 CCCTGGCTGTCC-TGGCACTCACTCTGTAGACCAGGCTGGCCTCAAACTCAGAAATCTGC 1657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                    1658 CIGCCICIGCCICCCAAAIGCIGGGAITAAAGGCIIGCAC 1697
                                        484 ctgcttgtgcttcccaagtgcttagattaaaggtgtgcac 523
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FILING DATE: 22-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 07/728,838
APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-May-1991
ATTONNEY/AGENT INFORMATION:
NAME: HARSON, NO. 5612201man D.
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                            Sequence 5, Application US/08299849B Patent No. 5612201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JMBER: 07/807,043
12-DECEMBER-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 07/764,364 FILING DATE: 23-SEPTEMBER-1991 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Felfe & Lynch STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic DNA
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Best Local Similarity 80.69
Matches 129; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SITY: New York City STATE: New York
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US-08-299-849B-5
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Length 1355;

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STATE: N
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APPLICANT: Tominaga, Akira
APPLICANT: Takagi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1355;
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                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,390
FILING DATE: 19910910
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0; Mismatches 35;
                                                                                                                                     ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08442282
Patent No. 5760204
                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: MISTOCK, S. LESIIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 700
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 212 869864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 78.4%;
Matches 131; Conservative
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APPLICANT: Takatsu, Kiyoshi
APPLICANT: Tominaga, Akira
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1355 base partition of TYPE: NUCLEIC ACID STRANDEDNESS: single
                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                  New York
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; LOCATION: 13...
US-07-757-390-16
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Takagi, Satoshi
Murata, Yoshiyuki
ENTION: Human And Murine Interleukin-5 Receptor
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APPLICANT: Takagi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1236 TCCCGTCTGTGCATCCCAGGTGCTGTATTAAAGGCGAGCTCTACCA 1190
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                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
JURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,282
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APPLICATION NUMBER: 07/757,390
FILING DATE: 10-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 78.4
Matches 131; Conservative
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MEDIUM TYPE: Floppy
                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennle &
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                                                                                                                                                                                                          E: New York
FRY: U.S.A.
10036-2711
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1295 AGCTCTGGCTGTCC-TGGAACTCACTTTATAGACCAAGCTGGCCTCGAACTCAGAAATCC 1237
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS.
SOFTWARE: Patentin Release #1.0, Version #1.25
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1155 Avenue of the Americas
                                                                              US/08/442,281
                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/757,390
FILING DATE: 10-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Application US/08442281 Patent No. 5807991 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             TIONALI MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERIA MATERI
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APPLICANT: Takagi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human An
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.5%;
Best Local Similarity 78.4%;
Matches 131; Conservative
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                                         CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & 1
STREET: 1155 Avenue
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
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                                                                                                                       FILING DATE
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APPLICANT: Takatsu, Kiyoshi
APPLICANT: Tominaga, Akira
APPLICANT: Takatyi, Satoshi
APPLICANT: Takatyi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1355;
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Pred. No. 2.3e-17;
0; Mismatches 35; Indels
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                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SURRIYAR APPLICATION DARA:
APPLICATION NUMBER: US/08/442,282
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                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/757,390
FILING DATE: 10-5EP-1991
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, 5. Leslie
REGISTRATION NUMBER: 18,72
REFERENCE/DOCKET NUMBER: 7005-030
TELEPHONE: 212 790-9090
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEFX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1355 base pairs
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Patent No. 5807991
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Best Local Similarity 78.4%;
Matches 131; Conservative
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STRANDEDNESS: single
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                                         COMPUTER READABLE FORM:
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13..1008
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MOLECULE TYPE:
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; LOCATION:
US-08-442-282-16
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422 agtectggetgteettggaaeteaetetgtagaeceaggetggeettgaaeteagaaatee 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35; Indels
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Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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Cambridge
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                                                                                    REFERENCE/DOCKET NUMBER: 70
ELECOMMUNICATION INFORMATION
TELEPHONE: 212 790-9090
                                                                                                                                           TELEFAX: 212 8698864/9741
TELEX: 66141.PENNIE
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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LaVallie, Edward
Racie, Lisa
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ATTORNEY/AGENT INFORMATION:
                                                        . Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.55
Best Local Similarity 78.45
Matches 131; Conservative
                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy
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13..1008
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA
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; LOCATION:
US-08-442-281-16
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374 tttggtttggttttgatttgtttatttgagacagggcttctctgtgtagtcctggctgt 433
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                                                                                                                                                                                                                                           434 ccttggaactcactctgtagaccaggctggccttgaactcagaaatccgcctgcttgtgc 493
                                                                                                                                                                                                                                                                                 458 CC.TARAACTCACTCTGTAGACCAGGCTGGCCTCGAACTCAGAATCTGCCCGCTTCTGC 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor NUMBER OF SEQUENCES: 18
                                                                   Length 535;
                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PPELICATION NUMBER: US/07/757,390
FILING DATE: 19910910
                                                             Score 96.2; DB 2;
Pred. No. 7.6e-17;
1; Mismatches 19;
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F: 1155 Avenue of the Americas
New York
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SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 84.9%;
Matches 118; Conservative
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ADDRESSEE: Pennie &
STREET: 1155 Avenue
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APPLICANT: Murata
TITLE OF INVENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'RY: U.S.A.
10036-2711
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US-08-686-878A-38
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1749 GGAACTCACTTTATAGACCAAGCTGGCCTCGAACTCAGAAATCCTCCCGTCTGTGCATCC 1690
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                                                                                                                  1808 GTTTGTTTGTTTGTTTTTTCGAGACAGGGTTTCTCTGTGTAGCTCTGGCTGTC-T 1750
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378 gtttggtttgagttttgttttatttgagacagggcttctctgtgtagtcctggctgtcctt 437
                                                                                          438 ggaactcactctgtagaccaggctggccttgaactcagaaatccgcctgcttgtgcttcc 497
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APPLICANT: Takagi, Satoshi
APPLICANT: Takagi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTOR Human And Murine Interleukin-5 Receptor
UNDBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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APPLICATION NUMBER: US/08/442,282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.4%; Score 94.2; DB 3; 1
Best Local Similarity 80.8%; Pred. No. 5.7e-16;
Matches 122; Conservative 0; Mismatches 28;
                                                                                                                                                                                                                            1689 CAGGIGCIGIATIAAAGGCGAGCICIACCA 1659
                                                                                                                                                                                   498 caagtgcttagattaaaggtgtgcactgcca 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CIIY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/757,390
FILING DATE: 10-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08442282
Patent No. 5760204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION TELEPHONE: 212 790-9090
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1808 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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                                                                                                                                                                                   378 gtttggtttgagttttgtttatttgagacagggcttctctgtgtagtcctggctgtcctt 437
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                                                                                   1.4%; Score 94.2; DB 1; Length 1808; 80.8%; Pred. No. 5.7e-16; tive 0; Mismatches 28; Indels 1
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APPLICANT: Takagi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,390
FILING DATE: 19910910
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5.7e-16;
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STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15, Application US/07757390 Patent No. 5453491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/COCKET NUMBER: 700
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SED ID NO: 15:
SEQUENCE CHARACTERISTICS:
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TTORNEY/AGENT INFORMATION:
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                                                                                        Query Match
Best Local Similarity 80.8%
Matches 122; Conservative
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
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Best Local Similarity
Matches 122; Conserva
CDNA
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; MOLECULE TYPE:
US-07-757-390-2
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US-07-757-390-15/C
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US-07-757-390-15
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Gaps

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Sequence 2, Application US/08442281
Patent No. 5807991
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ADDRESSEE: Pennie &
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URRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,282
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1.4%; Score 94.2; DB 3;
Best Local Similarity 80.8%; Pred. No. 5.7e-16;
Matches 122; Conservative 0; Mismatches 28;
                                                 1689 CAGGTGCTGGTATTAAAGGCGAGCTCTACCA 1659
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498 caagtgcttagattaaaggtgtgcactgcca 528
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STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                              Sequence 15, Application US/08442282
Patent No. 5760204
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/757,39
FULLING DATE: 10-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: MSIOCK, S. Leslie
RECISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 10,005
                                                                                                                                                                                                                                                 APPLICANT: Takatsu, Kiyoshi
APPLICANT: Tominaga, Akira
APPLICANT: Takagi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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TELEEX: 66141 PENNIE
INFORMATION FOR SEO ID NO: 15
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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303..1547
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; LOCATION:
US-08-442-282-15
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1808 GITIGITIGITIGITITITICGAGACAGGGITICICIGITAGCICIGGCIGICC-T 1750
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APPLICANT: Takatsu, Kiyoshi
APPLICANT: Tominaga, Akira
APPLICANT: Takagi, Satoshi
APPLICANT: Takagi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
NUMBER OF SEQUENCES: 18
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                                                                                                                                                                                                                                                                                        STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,281
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/757,390
FILING DATE: 10-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: MAJSTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005-030
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Patent No. 5807991
                                                                                                                                                                                                          E: Pennie & Edmonds
1155 Avenue of the 1
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TELEX: 66141 PENNIE
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACIERISTICS:
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APPLICANT:
APPLICANT:
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1749 GGAACTCACITIATAGACCAAGCTGGCCTCGAACTCAGAAATCCTCCGGTCTGTGCATCC 1690
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Murata, Yoshiyuki
VENTION: Human And Murine Interleukin-5 Receptor
EQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 94.2; DB 3; Length 1:
Pred. No. 5.7e-16;
0; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
UNRRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,281
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NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/757,390
FILING DATE: 10-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Lessie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005-030
TELECOMUNICATION INFORMATION:
TELEPAX: 212 790-9090
TELEPAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1808 base pairs
TYRE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 80.8%;
Matches 122; Conservative
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Search completed: September 28, 1999, 16:41:07 Job time: 7053 sec bcl-1 probe G13b. Hepatitis C virus

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ALIGNMENTS .

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

September 28, 1999, 16:50:24; Search time 303.81 Seconds (without alignments) 28.823 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-037-657-30 35 1 agctggcgcctcccgggcggatcgggagccac 35

IDENTITY_NUC Scoring table:

311585 seqs, 125096042 residues Searched:

N_Geneseq_36:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Result No.	П	7	m	4 (יטי		c 2	ω .	σ,	10		77.	٠,	+ t	٦.	9 -	7 .	٦, ۲-	100	ט פר	40		ייי	c 25	~	27	28	53	m	c 31	י ר	י ר	יי ר	2 6	יי נ	, ,	י ר) <	ב קל	7 4	7	•

RESULT 1 V27146 standard; DNA; 35 BP. DC V27146; DD V27146 standard; DNA; 35 BP. DD V27146 standard; DNA; 35 BP. DD V27146 DD V27146 EN V27146 EN V27146 EN V27146 EN WALSIP-1998 (first entry) EN WASS-1996 (first entry) EL SEP-1997; CALP primer; maplification. Synthetic. Mus sp. Synthetic. Mus sp. PP 11-SEP-1997; GO479. PP WO991125-A2. PP WO2127, DIRECLEWARA H E. PR ANRA-) ANRAD OPERATIONS PTY LTD. PR 11-SEP-1996; AU-002246. PR 11-SEP-1996; AU-002246. PR (AMRA-) ANRAD OPERATIONS PTY LTD. PR (AMRA-) ANRAD OPERATION PR (AMRA-) S. Willson T., PI (Adjuma T. Maeda M. Nash A. Nicola NA, Rakar S. Willson T., PI (Adjuma T. Maeda M. Nash A. Nicola NA, Rakar S. Willson T., PR (Adjuma T. Maeda M. Nash A. Nicola NA, Rakar S. Willson T., PR (Adjuma T. Maeda M. Nash A. Nicola NA, Rakar S. Willson T., PR (Adjuma T. Maeda M. Nash A. Nicola Na, Rakar S. Willson T., PR (Adjuma T. Maeda M. Nash A. Nicola Na, Rakar S. Willson T., PR (Adjuma T. Maeda M. Nash A. Nicola Na, Rakar S. Willson T., PR (Adjuma T. Maeda M. Nash A. Nicola Na, Rakar S. Willson T., PR (Adjuma T. Maeda M. Nash A. Nicola Natlation T., PR (Adjuma T. Maeda M. Nash A. Nicola Natlate S. Willson T., PR (Adjuma T. Maeda M. Nash A. Nicola Natlate S. Willson T., CE (Afferentiation and survival of a wide variety of cells. The Repolution and survival of a wide variety of cells. CC (Afferentiation and survival Nature and In vivo. They can be present in CC charapeutics used for modulating neuronal proliferation and survival. CC (Afferentiation and survival. The products can also be used for detection and survival. CC (Afferentiation and survival. The products can also be used for detection and survival. CC (Afferentiation and survival. The products can also be used for detection and survival. CC (Afferentiation and survival. The products can also be used for detection and survival. CC (Afferentiation and survival. The pr	Query Match Best Local Similarity 100.0%; Score 35; DB 1; Length 35; Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 agctggcgcctcccgggcggatcgggagccac 35	PF 11-SEP-1997, G02479. PR 11-SEP-1996; AU-002246. PA (AMRA-) AMRAD OPERATIONS PTY LTD. PA (PZIE) DZIEGLEWSK L. PA ALEXANDER W, Fabri L. Farley A, Hilton DJ, Kikuchi Y,
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217 CICGGGGIGCCICGGGGGGGGAICGGGAGCCCAC 249

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Claim 5; Page 84-87; 187pp; English.

Claim 5; Page 84-87; 187pp; English.

The haemopoletin receptor (HR) NR6.2 is a form of the novel HR NR6.

The haemopoletin receptor (HR) and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. cor cancers or predisposition to cancers, or for drug screening.
                                                                                                                                                                      Novel hamopoletin receptor NR6.2 gene. Hamopoletin receptor; cell proliferation; cell differentiation; cancer; ell survival; therapeutic; neuronal proliferation; drug screening; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-007-1998 (first entry)
Nucleotide sequence of the murine U4 gene.
Murine; U4 protein; haematopoletin receptor superfamily;
cell proliferation; immune response; antibody; cell differentiation;
autoimmune disease; cancer; allergy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated haemopoietin receptor - used for developing products for modulating proliferation, differentiation and survival of cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 1673;
                                                                                                                                                                                                                                                                                                                                                                "Haemopoietin receptor NR6.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y, Kojima I, Maeda M, Nash A, Nicola NA, Rakar S, Willson
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(GEMY ) GENETICS INST INC.
Collins M, Donaldson DD, Neben T, Whitters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.7%; Score 20.2; I 75.8%; Pred. No. 46; Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 CTCGGGGTGCCTCGGGGCGGATCGGGAGCCCAC 250
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/product= "U4 protein"
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1. .1278
/*tag= a
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(AMRA-) AMRAD OPERATIONS PTY LTD.
(DZIE/) DZIEGLEWSKA H E.
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                                                                                                      V27141 standard; cDNA; 1673
                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                   /product-
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L5-JAN-1998; U00334.
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Best Local Similarity
Matches 25; Conserva
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11-SEP-1997; G02479
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                                                                                                                               V27141;
29-SEP-1998
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Claim 4; Page 77-81; 182pp; English.
The haemopotetin receptor (HR) NR6.1 is a form of the novel HR NR6.
The haemopotetin receptor (HR) MR6.1 is a form of the novel HR NR6.
Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                      NRG is a novel haemopoietin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel hammopoletin receptor NR6.1 gene.
Haemopoletin receptor; cell proliferation; cell differentiation; cancer;
cell survival; therapeutic; neuronal proliferation; drug screening; ss;
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New isolated haemopoietin receptor - used for developing products
for modulating proliferation, differentiation and survival of cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
WPI; 98-260970/23.

New isolated haemopoietin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells

Example 8; Page 99-100; 182pp; English.
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Sequence 1629 BP; 336 A; 541 C; 453 G; 299 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMRA-) AMRAD OPERATIONS PTY LTD. (DZIE/) DZIEGLEWSKA H E. Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y, Kojima I, Maeda M, Nash A, Nicola NA, Rakar S, Willson
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60
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                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218 CTCGGGGTGCCTCGGGGCGGATCGGGAGCCCAC 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 ctggcgcgcccgggggggtcggggggccac 35
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Pred. No. 45
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75.8%;
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llarity 75.8%;
Conservative
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/*tag* a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                Query Match 57.7
Best Local Similarity 75.8
Matches 25; Conservative
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11-SEP-1996; AU-002246.
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Best Local Similarity
Matches 25; Conserv
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29-SEP-1998
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Mus sp. Mouse.

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Gaps

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Treat, mover and encoding U4 haematopoietin receptor superfamily chain - potentially useful, e.g. for modulating cell proliferation or I munue response, for treating cancer and auto:immune.disease Claim 1; pages 25-26; 38pp; English.

This is the nucleotide sequence encoding the murine U4 protein from the haematopoietin receptor superfamily, used in the method of the cinvention for the modulation of cell proliferation, or the immune response. Transformed mammalian cells are used to produce recombinant U4 protein. The U4 protein is used to screen for specific binding as tissue markers for isolation of cognate ligands and receptors, and in pharmaceutical compositions which may modulate cell proliferation, cell differentiation, and the immune system (e.g. for treating immune diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 72-75; 55pp; English.

Disclosure; Page 72-75; 55pp; English.

The present sequence encodes a protein designated Zeytor5, which is a cytokinin-like receptor. Soluble Zeytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart of cardiotrophin-1 on cardiac pathologies, so preventing heart blood, and to discover other possible Zeytor5 ligands. A probe comprising Zeytor5 DNA or RNA can be used to determine the presence and integrity of the Zeytor5 gene on chromosome 19. Antibodies and the cardiotrophia antibody could be used to purify Zeytor5 and therapeutically to modify Zeytor5 ligand effects.

Sequence 1724 BP; 350 A; 550 C; 500 G; 324 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-MAR-1999 (first entry)

CDNA encoding rat Zcytor5.

Zcytor5; cytokinin-like receptor; down-regulation; growth factor; maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1; cardiac pathology; heart enlargement; Zcytor5 ligand; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g. down-regulating Zcytor5 natural ligands or detecting cardiotrophin-l
                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 1656;
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Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
Lok S, Presnell SR, Whitmore TE;
                                                                                                                                                                                                                                                                                                                                                478 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 CTCGGGGTGCCTCGGGGCGGATCGGGAGCCCAC 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 ctggcgcgctcccgggcggatcgggagcccac 35
                                                                                                                                                                                                                                                                                                                                                552 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
159. .1436
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/product= 2cytor5
                                                                                                                                                                                                                                                                                                                                              318 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V70896 standard; cDNA; 1724
                                                                                                                                                                                                                                                                                                                        cancer, and allergy).
Sequence 1656 BP;
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01-MAY-1997; US-850030
13-FEB-1998; US-023890
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P-PSDB; W70862.
                      P-PSDB; W59804
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|3-FEB-1998;
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V70896
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Gaps
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O78165/C

ID 078165.

AC 078165.

D7 07-3010-1995 (first entry)

DE U149 homologue gene of bovine herpes virus 1 (BHV-1)

KW Cattle pathogen; infectious bovine rhinotracheitis; nucleocapsid;

KW VP4; promoter; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mutant bottne herpes type 1 virus with deleted gene(s) - used as vaccine, also with replacement bacterial or viral pathogen branches also with replacement bacterial or viral pathogen and/or cytokine(s), inserted at deletion brample; Fig 11: 109pp; English.

Q78165/R63461 are the nucleotide sequence and deduced AA sequence of BHV 1 UL49 homologue gene. The complete DNA sequence between the Namologue gene and dUTPase gene (UL50 homologue) gene are presented, putative G-C box, TATA box and polyA signal sequence are indicated in FT. The boundaries of UL50, UL 49.5 and UL48 ORFs surrounding the UL 49 homologue gene are also indicated. Sequence complete the complete of UL50, UL 49.5 and UL48 ORFs surrounding the UL 49 homologue gene are also indicated.
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                           Length 1724;
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Human oxygen regulated protein ORP 150 gene promoter.
Oxygen regulated protein; ORP 150; stress protein; ischaemia;
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/label= dUTPase (UL50) ORF start codon
                           DB 1;
                           Score 20.2;
Pred. No. 46;
                                                                                          0; Mismatches
                                                                                                                                                                                           252 CTCGGGGTGCCTCAGGCGGGATCGGGAGCCCAC 284
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                                                                                                                                                  3 ctggcgcgctcccgggcggatcgggagcccac 35
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complement (28. .26)
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label= UL49.5 gene
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/label= UL48 ORF
                    57.7%;
75.8%;
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WPI; 94-341875/42.
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/*tag= e
1226 .1231
/*tag= f
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illarity 73.5%;
Conservative
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*tag*
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/*tag= c
Ouery Match
Best Local Similarity 75.8
Watches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-APR-1994; CA0201
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Best Local Similarity
Matches 25, Conserv
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Length 6306;

DB 1;

Score 19.2; Pred. No. 8

Pred.

us-09-037-657-30.rng

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mat_peptide
                           Query Match
Best Local S:
Matches 21
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Claim 24, Page 56-66, 93pp; English.

Claim 24, Page 56-66, 93pp; English.

MII and MT2 proteins were isolated from malignant cells essentially following the method of Penman and Fey, described in US Pat. Nos. 4, 200 and 4, 885,236. DNA sequences encoding these proteins were cloned by probing expression libraries using monoclonal antibodies raised against the isolated INM proteins. The genetic sequence coording MT2 has been disclosed by Yang et al. 1992, J. Cell Biol. 116:1395-1408, and is referred to by them as 'NuMA'. The nucleotide sequence encoding MT1 has not been described previously. Both the MT2 proteins are distributed throughout the nucleus (with the exception of the nucleolus) in non-mitotic cells, and localise to the exception of the nucleolus) in non-mitotic cells, and localise cell type in a sample which uses a mRNA complementary to 054841 is claimed.
                                                                                                                                                           craim 15; Page 45-47; Sipp; English.

C A genomic DNA molecule (164785) comprises the promoter region of the human oxygen regulated protein ORP 150 gene. It was obtd. from c human placenta genomic library using probes based on human and c rat ORP 150 cDNA clones (see also 764783 and 764784). The sequence c covers the 5' untranslated region to just before the translation c initiation codon in exon 2. It is able to promote transcription in cells when exposed to hypoxia, and will be useful for analysis of the corresponding human gene, partic. for facilitating its appln. C to the treatment of ischaemia diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                    The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-UUL-1994 (first entry)
Sequence encoding inner nuclear matrix (INM) protein MT2
Malignant cell type marker; interior nuclear matrix; MT2; NuWA; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel malignant cell type markers of the interior nuclear matrix used for detecting abnormal cell types e.g. malignant breast, prostate, lung, etc., for determining deg. of cell death in
                                                                                                                                           Human and rat oxygen regulated protein ORP 150 coding sequences useful in diagnosis and treatment of ischaemic diseases such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  924 T;
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                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 2861;
hypoglycaemia; hypoxia; gene therapy; diagnosis; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                              9; Indels
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                                                           20-DEC-1996; 120662.
20-DEC-1995; JP-349661.
23-JUL-1996; JP-213181.
(HSPR-) HSP RES INST INC.
HReda J, Kaneda S, Matsumoto M, Yanagi H, Yura T;
WPI: 97-322148/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2053 AGCGTGCGAGCTCCGGGGGCGGGTCGGGAGCGCA 2086
                                                                                                                                                                                                                                                                                                                                                                                 Score 19.6; DE Pred. No. 69; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 agetggegegetecegggeggategggageea 34
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1. 6306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q54841 standard; cDNA; 6306 BP
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 73.5%;
Matches 25; Conservative
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Lidgard GP, Toukatly G;
WPI; 94-026210/03.
P-PSDB; R47143.
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US-901701.
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e 6306 BP;
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Q54841
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The sequences given in T77782-83 encode fusion proteins which contain Twa sequences given in T77782-83 encode fusion proteins were used in NuMA (nuclear mitotic apparatus).

The fusion proteins were used in the fusion proteins were used in the identification of NuMA interecting proteins (NIP's) (see also W21729-30).

W21729-30). Compounds which interfere with the interaction of NuMA by traised conventionally using NIP-1 or -2 as immunogen, are used to detect NIP (or their complexes) and to block their activity for detect NIP (or their complexes) and to block their activity for which may be markers for aberrant (including malignant) cell growth (which can also be detected by nucleic acid sequencing). Also where
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                                                                                                                                                                                                                                                                                                                                                                                           cDNA encoding (ALA/HANNUMA fusion protein.

NIP-1; NIP-2; NuMA; nuclear mittotic apparatus; NuMA interacting protein;
ell division; proliferation; antibody; Ab; detection;
malignant cell growth; ss.

Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          malignancy is related to defects in NuMA or NIP, it can be treated by administration of the appropriate functional protein. Sequence 6819 BP: 1796 A; 1841 C; 2136 G; 1046 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding nuclear mitotic appts. interacting proteins - useful for modulating cell division and proliferation and
                                                        Gaps
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                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= Residues 18-2116 of NuMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product GAL4 DNA binding domain 442. .522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= b
/product= hemaglutinin tag
                                                        0; Mismatches
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cDNA encoding Lexa/NuMA fusion protein.
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1. .441
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                                                                                                              6 gogogottocogggoggatoggga 29
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                                                                                                                                                                                                                                                                                                                      I77782 standard; cDNA; 6819 BP.
ch 54.9%;
1 Similarity 87.5%;
21; Conservative
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07-JUN-1996; U09504.
07-JUN-1995; US-478408.
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01-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
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411 T;

672 G;

751 C;

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picciosure; Page 58-61; 112pp; English.

The nucleotide and deduced as sequences of human transducin-like enhancer of split proteins TLE-1 (062175, R51476), TLE-2 (062176, R51477), TLE-3 (062177, R51478) and TLE-4 (062178, R51479) were determined. The as sequences were compared with that of Drosophila E(spl)m9/10 protein (R51481). Comparison of the WD-40 domains of these proteins defined the consensus residues shown in R51480. The antigen, human c-myc, human p53, human A-myb and dorsal proteins with respect to nuclear localization site, and casein-kinase II and cdc2-kinase phosphorylation sites (sequences R51482-96). TLE can be
                    associated multi-protein complexes, chimeric proteins,
antibodies, nucleic acid, etc., involved in nuclear-cytoplasmic
protein transport
                                                                                                                                                                                                                                                                                                                                                                                               54.3%; Score 19; DB 1; Length 2271; llarity 71.4%; Pred. No. 1.1e+02; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                               used to treat or diagnose (pre)neoplastic conditions, or to study cell differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 agctggcgcgtcccgggcggatcgggagccac 35
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Best Local Similarity
Matches 25; Conserva
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Claim 16; Page 42-50; 78pp; English.

The acquences given in T7782-83 encode fusion proteins which contain

The sequences given in T7782-83 encode fusion proteins which contain

The identification of NuMa interecting proteins (NIP'S) (see also

W21729-30). Compounds which interfere with the interaction of NuMa

W21729-30. Compounds which interfere with the interaction of NuMa

X2 Ab, raised conventionally using NIP-1 or -2 as immunopen, are used to

detect NIP (or their complexes) and to block their activity for

C diagnostic or therapeutic use, e.g. to detect defective NuMa or NIP

C which may be markers for aberrant (including malignant) cell growth

C which can also be detected by nucleic acid sequencing). Also where

C malignancy is related to defects in NuMa or NIP, it can be treated by

C administration of the appropriate functional protein.
        apparatus; NuMA interacting protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding nuclear mitotic appts. Interacting proteins – useful for modulating cell division and proliferation and
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protein transport; cervix cancer; dysplasia; malignancy;
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NIP-1; NIP-2; NuMA; nuclear mitotic apparatus; NuMA in cell division; proliferation; antibody; Ab; detection; malignant cell growth; ss.
                                                                                                                                                                                                                                                            /product= Residues 18-2116 of NumA
                                                                                                                                           /product= LexA DNA binding domain 262. .283
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                                                                                  Location/Qualifiers
                                                                                                                                                                                  /*tag= b
/note= "Polylinker"
284. .6579
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26. .2257
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062176/C
ID 062176;

AC 062176;
DT 10-SEP-1994 (first entry)
DE Human TLE-2 gene.
KW TLE-2; transducin-like enhancer of protein transport; cervix cancer;
KW TLE-2; transducin-like enhancer of protein transport; cervix cancer;
KW TLE-2; transducin-like enhancer of protein transport; cervix cancer;
KW TLE-2; transducin-like enhances
KW TLE-2; transducin-like enhances
KW TLE-2; transducin-like enhances
KW TLE-2; transducin-like enhances
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                                                                                                                        /*tag= a
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                                                                                                      .261
                                                                                                                                                                                                                                                                                                               07-JUN-1996; U09504.
07-JUN-1995; US-478408.
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Best Local Similarity
Matches 21; Conserv
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                                                               Homo sapiens
                                                                                                misc_feature
                                                                                                                                                             misc_feature
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are for treatment of disorders of cell fate or differentiation
T. G. cervical cancer, breast cancer, psoriasis, baldness etc.
Disclosure: Page 91-94, 147pp; English.
The nucleotide and deduced as sequences of human transducin-like enhancer of split proteins TLE-1 (04533, R51109), TLE-2 (045334, R5110), TLE-3 (045335, R51110), TLE-2 (045334, CELL), TLE-2 (045336, R52935), CELL R5110), TLE-3 (045336, R52935), CELL R5110), TLE-3 (045336, R52935), CELL R5110, TLE-3 (045336, R52955), CELL R5110, TLE-3 (045336, R52955), CELL R5110, TLE-3 (045336, R52955), CELL R5110, TLE-3 (045336, R52956, CELL R5110, TLE-3 (045336, R52956, CELL R5110, TLE-3 (045336, R52956, CELL R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (045336, R5110, TLE-3 (04536, R5110, TLE-3 (04536, R5110, TLE-3 (04536, R5110, TLE-3 (04536, R5110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human TLE-2 gene.
TLE-2; transducin-like enhancer of split protein; cell fate,
differentiation; cervix cancer; breast cancer; psoriasis; baldness;
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Pred. No. 1.1e+02;
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Sequence 2271 BP; 437 A; 751 C; 672 G;
1896 AGCIGGGGCCCTCCCGCAGGTCCCAGCAGCCCAC 1862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1896 AGCTGGCGCCCTCCCGCAGGTCCCAGCAGCCCAC 1862
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54.3%; Score 19; DB

Best Local Similarity 71.4%; Pred. No. 1.1e

Matches 25; Conservative 0; Mismatches
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WPI; 94-135221/16.
P-PSDB; R51110.
                                                                                                                                                            RESULT 13

Q45334,C

DQ G45334 standard; CDNA; 2271 BP. O45334;

DT 10-SEP-1994 (first entry)

E Human Tibe.2; transducin-like enhances:

KW Tibe.2; transducin-like enhances:

KW Gifferentiation; cervix cancer;

KW Gifferentiation; cervix cancer;

KRY SS.

COALION/QUallif

FT Key 26. .2257

FT CAS .2257

FT WO940752-A.

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Mycobacterium tuberculosis genomic DNA fragment (I). Tuberculosis; mycobacteria; infection; diagnosis; antimycobacterial; antiblotic; vaccine; ss.

Mycobacterium tuberculosis WO9741252-A2.

T93610 standard; DNA; 3946 BP 27-APR-1998 (first entry) 06-NOV-1997. 18-APR-1997; E01973. 18-APR-1996; DE-017184. (GBPB) GBF GES BIOTECH FORSCHUNG GMBH. ESPITIA C, Honlsch C, Moreno C, Singh M;

WPI; 97-549750/50 P-PSDB; W31852-55

us-09-037-657-30.rng

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New Particle of Materials of RNA derived from M. tuberculosis - used for diagnosis of mycobacterial infections, monitoring used for diagnosis of mycobacterial infections, monitoring used for diagnosis of mycobacterial infections, monitoring used for diagnosis of mycobacterial agents

T vectination and development of anti-mycobacterial agents
Claim 1; Fig 9; 55pp; English.

Claim 1; Fig 9; 55pp; English.

New claimed DNA (A) has one of 3 isolated Mycobacterium

Cuberculosis DNA sequences of 3946 bp (I) (T93610), 2653 bp (VI)

Claim 1; Fig 9; 55pp; English.

Claim 2; Fig 9; 55pp; English.

Claim 2; Fig 9; 55pp; English.

Claim 2; Fig 9; 55pp; English.

Claim 4; Fig 9; 55pp; English.

Cloim 4; Fig 9; 55pp; English.

Cloim 5; Fig 9; 55pp; English.

Cloim 6; My and proteins encoded by (A). To isolate probes of a protein cloim 2; Fig 9; Fig 9; Fig 9; Fig 9; Fig 9;

Cloim 6; Fig 9; 55pp; English.

Cloim 6; Fig 9; 
Cloim 6; Fig 9; 
Cloim 6; Fig 9; 
Cloim 6; Fig 9; 
Cloim 6; Fig 9; Fig 9; Fig 9; Fig 9; Fig 9; Fig 9;

Cloim 6; Fig 9; Fig 9; Fig 9; Fig 9; Fig 9;

Cloim 6; Fig 9; Fig 9; Fig 9; Fig 9;

Cloim 6; Fig 9; Fig 9; Fig 9; Fig 9;

Cloim 6; Fig 9; Fig 9; Fig 9; Fig 9;

Cloim 6; Fig 9; Fig 9; Fig 9; Fig 9;

Cloim 6; Fig 9; Fig 9; Fig 9; Fig 9;

Cloim 6; Fig 9;

Cloim 
                                                     r93610,
RESULT
                                                                                                                                             naturally produce claving.

Disclosure; Fig.2; 41pp; English.

A library of S. claviligerus NRRL 5741 genomic DNA fragments (15-22 kb) constructed in cosmid pLAFR3 was screened for the cla gene using a probe based on a partial N-terminal sequence from the CLA enzyme. Isolated clone KGil included a lSkb fragment having the sequence given in Q91580 that included the cla gene (ORF4).
                                                                                                                                                                                                                           13-NoV-1995 (first entry)
S. clavuliniderus cla gene region.
Clavulinic acid; clavulinate; antibiotic; beta-lactamase-inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aldoo KA, Jensen SE, Paradkar AS;
WPI: 95-207301/28.
P-PSDB: 877865; R77869; R77861; R77862; R77863; R77864;
R77865; R77866; R77867.
R77865; R77866; R77867.
R77865: R77866; R77867.
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Best Local Similarity 76.7%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 7;
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complement (49 .1745)
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611. .7588
                                                                                                                                                                                              Q91580 standard; DNA; 15079 BP.
Q91580;
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/label= ORF10
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13769. .14995
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label= ORF8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces clavuligerus
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08-OCT-1993; 108113.
08-OCT-1993; CA-108113.
(UYAL-) UNIV ALBERTA.
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Gaps
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                                                                                               Length 3946;
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as for epidemiological studies, for monitoring vaccinations development of anti-mycobacterial drugs and vaccines Sequence 3946 BP; 518 A; 1541 C; 1345 G; 5
                                                                                               53.7%; Score 18.8; DB 1; 76.7%; Pred. No. 1.2e+02; tive 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                     Search completed: September 28, 1999, 16:50:28
Job time: 7613 sec
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Best Local Similarity
Matches 23; Conserva
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Matches
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Gaps

7; Indels

Db 13682 GCGCGCCCCCGGCGGACCGGCCACCCGC 13711 6 gegegeeteeegggeggategggageeeae 35

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Length 15079;

us-09-037-657-30.rni

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37 ; Search time 152.56 Seconds
(without alignments)
21.032 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
                                                                                                                             September 28, 1999, 16:41:07
                                                                               OM nucleic - nucleic search, using sw model
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1 agctggcgcctcccgggcggatcgggagcccac 35 US-09-037-657-30 35 Title: Perfect score: Sequence:

IDENTITY_NUC Scoring table:

176461 segs, 45838279 residues

Searched:

/cgn2_6/ptodata/2/1na/5B_COMB.seq:*
/cgn2_6/ptodata/2/1na/5C_COMB.seq:*
/cgn2_6/ptodata/2/1na/5D_COMB.seq:*
/cgn2_6/ptodata/2/1na/Pcru59_COMB.seq:*
/cgn2_6/ptodata/2/ina/Packfiles1.seq:* /ptodata/2/ina/5A_COMB.seq:* Issued_Patents NA:* Database ::

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SOTWARE: PC-DOS/MS-DOS
SOTWARE: Patentin FC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 06-JUN-1995
CLASIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REGISTRATION MUBBER: 27 829
REFERENCE/DOCKET WINBER: 27 829
REFERENCE/DOCKET WINBER: TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6306 base pairs

LENGTH: 6306 base pai TYPE: nucleic acid STRANDEDNESS: single

TOPOLOGY: linear MOLECULE TYPE: CDNA

E: Floppy disk IBM PC compatible

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d1
COMPUTER: IBM PC compa
OPERATING SYSTEM: PC-D
SOFTWARE: Patentin Rel

USA

STATE: M COUNTRY:

02110

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		Description	Sequence	Segmence	Sequence	Segmented	Sections	Secretary	Segmenter	Sequence	Segmence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	ednence	
SUMMARIES		qi	-466-390	US-08-470-950-3	US-08-467-781-3	US-08-195-487-3	US-08-483-924-3	PCT-US93-06160-3	US-08-681-129-1	US-08-555-669-11	US-08-102-863-10	PCT-US92-10885-10	US-08-125-468-1	US-08-474-933-1	US-07-947-120-7	US-07-947-120-9	US-08-173-508-7	US-08-472-893A-7	US-08-472-893A-9	US-08-306-691B-51	US-08-460-694-1	US-08-464-517-1	US-08-464-517-34	US-08-804-227C-7	JS-08-290-665A-124	PCT-US93-05000-1	PCT-US93-05000-34	PCT-US93-05000-36	PCT-US93-06251-51	PCT-US95-10398-124	JS-08-795-868-15	PCT-US95-06137-1	PCT-US95-06137-3	US-08-399-646-3	-08-399-646-	-08-607-	-08-607-321-	-07-642-734C	US-08-961-240-3
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	Query	Length	6306	9089	6306	6306	9089	6306	1578	2543	1735	1735	30001	30001	4221	476	1820	4221	476	1325	4244	1325	1317	44377	573	1325	1317	1317	2611	5/3	2614	685	685	1791	2026	1791	2056	11219	1791
d	Query	Match	54.9	54.9	54.9	54.9	54.9	54.9	53.1	53.1	52.6	52.6	52.0	52.0	50.9	50.9	20.0	50.0	50.9	50.0	50.9	50.9	50.9	50.6	50.0	50.9	9.00			900	200	۳. د د د د	50.3	49.7	49.7	49.7	49.7	49.7	49.7
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Gaps

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Score 19.2; DB 2; Length 6306; Pred. No. 44; 0; Mismatches 3; Indels 0

Conservative

Query Match Best Local Similarity Matches 21; Conserv

US-08-466-390-3

: CLEVELAND DON W PRIMARX STRCTURE OF NUMA, AN INTR PROTEIN THAT DEFINES A NOVEL PATHW SEGREGATION OF PROTEINS AT MITOSIS

TITLE: P TITLE: S TITLE: S JOURNAL: AUTHORS:

COMPTON, DUANE A SZILAK, ILYA

AUTHORS: AUTHORS:

LOCATION: 1.6306 PUBLICATION INFORMATION

NAME/KEY: CDS

Sequence 13, Appl Sequence 3, Appl1 Sequence 13, Appl Sequence 1, Appl1 Sequence 1, Appl1 Sequence 18, Appl	Sequence 1, Appli	MARKERS OF THE
US-08-961-240-13 US-08-605-501-3 US-08-605-501-13 PCT-US93-08386-3 US-08-136-277-1 US-08-136-277-1 US-08-255-471-8	US-08-479-403-1 ALIGNMENTS	US/08466390 GARY GRAHAM P NOVEL MALIGNANT CELL TYPE MARKERS INTERIOR NUCLEAR MATRIX 6 S: S: HEBET
C 38 17.4 49.7 2056 4 C 40 17.4 49.7 2056 4 C 41 17.4 49.7 2056 4 C 41 17.4 49.7 1500 5 C 43 17.2 49.1 1250 2 C 44 17.2 49.1 1448 2	c 45 1/.2 49.1 2750 4	RESULT 1 US-08-466-390-3 Sequence 3, Application US/08466390 Patent No. 5868562 GENERAL INFORMATION: APPLICANT: TOURALLY, GARY APPLICANT: LIDGARD, GRAHAM P TITLE OF INVENTION: NOVEL MALIGN TITLE OF INVENTION: INTERIOR NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS: ADDRESSE: TESTA, HURMIT & THE STREET: 125 HIGH STREET CITY: BOSTON STAFF: MAD STREET STREET: 125 HIGH STREET STREET: MAD STREET STREET: MAD STREET STREET: MAD STREET STREET: MAD STREET

us-09-037-657-30.rni

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APPLICANT: TOURATILY, GARY
APPLICANT: LIDGARD, GRAHAM F
ITILE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 125 HIGH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDGARD, GRAHAM P
NTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,781
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3459 GCGGCCTCCCGGGCTGAGCGGGA 3482
                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY-AGENT INFORMATION:
NAME: PITCHER ESQ. EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MIP-
TELECOMMUNICATION:
Sequence 3, Application US/08467781 Patent No. 5780596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pplication US/08195487
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Best Local Similarity 87.5%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (617) 248-70
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                        ZIP: 02110
COMPUTER REDABLE FORM:
MEDIUM TYPE: F1
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PUBLICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LIDGARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                       BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS:
AUTHORS:
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                                                                                                                                                                                                                                              TYPE MARKERS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : CLEVELAND, DON W
PRIMARY STRUCTURE OF NUMA, AN INTRANUCLEAR
PROTEIN THAT DEFINES A NOVEL PATHWAY FOR
SEGREGATION OF PROTEINS AT MITOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,950
FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
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                                                                                                                                                                                                APPLICANT: TOUKATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TY.
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                   E: TESTA, HURWITZ & THIBEAULT
125 HIGH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 3459 GCGGCCTCCCGGCTGAGCGGGA 3482
                                       3459 GCGGGCTCCCGGGCTGAGCGGGA 3482
                                                                                                                                       Sequence 3, Application US/08470950
Patent No. 5698439
    6 gcgcgcctcccgggcggatcggga 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: PITCHER ESQ, EDMUND R REGISTRATION NUMBER: 27,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: M
TELECOMMUNICATION INFORMATION
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 87.55
Matches 21; Conservative
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PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
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                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS:
                                                                                                    RESULT 2
US-08-470-950-3
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Gaps

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RESULT

DB 3; Length 6306; Indels

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APPLICANT: TOUKATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 6306;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,487
INTERIOR NUCLEAR MATRIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIMARY STRUCTURE OF OF NUMA, AN IN PROTEIN THAT DEFINES A NOVEL PATHM. SEGREGATION OF PROTEINS AT MITOSIS: JOURNAL OF CELL BIOLOGY
                                                               ADDRESSEE: TESTA HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                       FILING DAYE:
CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/901,701
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MP-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7000
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                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 3459 GCGGCCTCCCGGCTGAGCGGGA 3482
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Patent No. 5882876
GENEZL INFORMATION:
APPLICANT: TOURATLY, GARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 87.5%;
Matches 21; Conservative
                                                                                                                                                                                  ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1.6306
UBLICATION INFORMATION:
                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; DATE: MAR-1992
US-08-195-487-3
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                                                                                                                                                                   COUNTRY:
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Sequence 3, Application PC/TUS9306160
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
CORRESPONDENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: TESTA HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                 COMPUTER: EACTS.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,924
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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                                                                                                                                                                            FILING DATE: 07-70N-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ. EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 246-7000
                                                                                                                                                                                                                                                                                                                        TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FON SEQ ID NO: 3.
SEQUENCE CHARACTERISTICS:
LENGTH: 6306 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 87.5
Matches 21; Conservative
COUNTRY: USA
21P: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1. 6306
PUBLICATION INFORMATION
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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MOLECULE TYPE: CDNA
FEATURE:
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OPERATING SYSTEM:
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DB 3; Length 1578;
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APPLICANT: Mayne, Richard
APPLICANT: Mayne, Richard
TILLE OF INVENTION: TYPE IX COLLAGEN AND FRAGMENTS THEREOF
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/555,669 FILING DATE: 13-NOV-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/08555669 Patent No. 5773248
                                                                                                                                                                                                                                                                                                   Pseudorables virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: PA+cn+T-
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TELEPHONE: 415-854-3660
                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Halluin, Albert F
REGISTRATION NUMBER: 25
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 72.73
Matches 24; Conservative
                                                                                          TELECOMMUNICATION INFORMA
TELEPHONE: (301) 258-5
INFORMATION FOR SEQ ID NO:
                                                    NAME: Gormley, Mary E. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: New York
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                                                                                                                                                                                                                                                                                                       ORGANISM:
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US-08-681-129-1
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Patentin Release #1.0, Version #1.25
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APPLICANT: Mettenleiter, Thomas Cristoph
TITLE OF INVENTION: Pseudorables virus vaccine
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Organon Teknika Corporation
STREET: 1330 Piccard Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19.2;
                  19930621
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APPLICATION NUMBER: 08/244,446
FILING DATE: 02-JUN-1994
CLASSIFTCATION: 424
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                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 3:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
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                    CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                     nucleic acid
EDNESS: single
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PUBLICATION INFORMATION
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                         APPLICATION NUMBER:
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Best Local Similarity
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LOCATION:
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Gaps
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           Length 2543;
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         DB 3;
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                                                                                                     1048 crrcccegecrrccragaccaccececrcaa 1080
     53.1%; Score 18.6; I
72.7%; Pred. No. 76;
ive 0; Mismatches
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Pred. No. 93;
0; Mismatches
                                                                                                                                                                                                                                                                TITLE OF INVENTION: CONSTITUTIVE
TITLE OF INVENTION: EXPRESSION OF P450SOY
TITLE OF INVENTION: AND FERREDOXIN-SOY IN
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                       2 gctggcgcgctcccgggcggatcgggagccca 34
                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: E. I. DU PONT DE NEMOURS
ADDRESSEE: AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: GALLEGOS, R. THOMAS
REGISTRATION NUMBER: 32,692
REFERENCE/DOCKET NUMBER: CR-9000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-7342
INFORMATION FOR SED ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  738 GCGACTCCTGCGCGGGCCCGGGAGCCGAC 765
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APPLICATION NUMBER: US/08/102,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/807,001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 19898
COMPUTER READABLE FORM:
ABDIUM TYPE: Floppy disk
CMEMUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                               Sequence 10, Application US/08102863 Patent No. 5466590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                              1007 MARKET STREET
                                                                                                                                                                                                                                                     SARIASLANI, SIMA
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78.6%;
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Query Match
Best Local Similarity 72.7
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 AND COMPANY
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Best Local Similarity 78.6°
Matches 22; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: ""C
                                                                                                                                                                                                                                                                                                                                                                                                                                WILMINGTON
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    MOLECULE TYPE:
US-08-102-863-10
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PCT-US92-10885-10
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APPLICANT: Ryan, Michael J.
APPLICANT: Ryan, Michael J.
APPLICANT: Ectvin, Jason A.
APPLICANT: Strathy, Nancy
APPLICANT: Fantini, Susan E.
TITLE OF INVENTION: Cloning of the biosynthetic pathway for
TITLE OF INVENTION: chlortetracycline and tetracyline Formation and cosmids
TITLE OF INVENTION:
TITLE OF INVENTION:
AUTHER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSED: American Cyanamid Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1735;
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Pred. No. 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Macintosh OPERATING SYSTEM: Macintosh System, 6.0 SOFTWARE: MICROSOff Word, 4.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10885
FILING DATE: 19921216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
TITLE OF INVENTION: CONSTITUTIVE
TITLE OF INVENTION: EXPRESSION OF P450SO
TITLE OF INVENTION: STREPTOMYCES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS: 12
ADDRESSEE: E. I. DU PONT DE NEMOURS
ADDRESSEE: AND COMPANY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 19898
COMPUTER REALBELE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
MEDIUM TYPE: 1.0 MB
                                                                                                                                                                                                           LOS:

LECT: LOT PONT DE CITY: WILMINGTON STATE DELAWARE COUNTRY: USA ZIP: 19898

ZIP: 19898

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ATTORNEY/AGENT INFORMATION:
NAME: GALLEGOS, R. THOMAS
REGISTRATION NUMBER: 32,692
REFRENCE/DOCKET NUMBER: CR-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-7342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08125468
Patent No. 5589385
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Best Local Similarity 78.6%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 302-892-7949
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEIC ACID
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STATE: New Jersey
COUNTRY: USA
ZIP: 07470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
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Gaps

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Indels

DB 4; Length 30001;

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Score 17.8; DB 1; Length 4221; Pred. No. 1.38+02; 0; Mismatches 7; Indels 0
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Patent No. 5538846
GENERAL INFORMATION:
APPLICANT: Meeker, Timothy C.
TITLE OF INVENTION: BCI-1 Locus Nucleic Acid Probes and
TITLE OF INVENTION: Assay Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/947,120 FILING DATE: 19920917 CLASSIFCATION: 435 ATTORNEY/ACTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Leona L. Lauder
STREET: Steuart Street Tower, 18th Fl., One Market
STREET: Plaza
                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 26694 Accresacecercesseacescenses 26664
                                                                                                                                                                                                                                                                  Score 18.2;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                            1 agctggcgcgcctcccggggcggatcgggagc 31
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REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-777-9257
TELEFAX: 415-543-4219
                                                                                                                                      DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 75.9%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                     52.0%;
ilarity 74.2%;
Conservative
30001 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1(
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. 1
                                                                      single
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                                      nucleic acid
                                                                                                          inear
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 23; Conserv
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                                                               STRANDEDNESS:
                                                                                                      TOPOLOGY: 11:
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HYPOTHETICAL:
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; LOCATION:
US-07-947-120-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JS-07-947-120-7/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                      US-08-474-933-1
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STATE:
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APPLICANT: Lotvin, Jason A.
APPLICANT: Strathy, Nancy
APPLICANT: Fantini, Susan E.
TITLE OF INVENTION: Cloning of the biosynthetic pathway for
TITLE OF INVENTION: chlortetracycline and tetracyline Formation and cosmids
TITLE OF INVENTION: useful therein
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                                      PatentIn Release #1.0, Version #1.25
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,933
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Pred. No. 77;
0; Mismatches
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                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,468
FILING DATE: 22-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TSev60s, Estelle J
REGISTATION NUMBER: 31,25-02
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,468
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08474933 Patent No. 5866410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 74.2%;
Matches 23; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 30001 base pairs
nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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New Jersey
XY: USA
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US-08-474-933-1/C
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STRAINS FOR EXPRESSION OF PEPTIDES AND
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                                                                          APPLICANT: Meeker, Timothy C.
TITLE OF INVENTION: BC1-1 Locus Nucleic Acid Probes and
TITLE OF INVENTION: Assay Methods
NUMBER OF SOUTENCE: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
                                                                                                                                                                                                                                                                                   COUNTRIES TO SHALE TORM:

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/947,120

TTT NG DATE: 19320917
                                                                                                                                                                                     ADDRESSEE: Leona L. Lauder
STREET: Steuart Street Tower, 18th Fl., One Market
STREET: Plaza
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Patent No. 5616485
GENERAL INFORMATION:
APPLICANT: Barffeld, Daniel
APPLICANT: Butler, Michael J.
APPLICANT: Butler, Michael J.
APPLICANT: Butler, Michael J.
APPLICANT: Genish, David
APPLICANT: Krieger, Timothy
TITLE OF INVENTION: STREPTOMYCES P
TITLE OF INVENTION: POLYDEPTIDES
WINDER
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FENTION: STREPTOMYCES
FENTION: STREPTOMYCES
FENTION: POLYPEPTIDES
                     Sequence 9, Application US/07947120
Patent No. 5538846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,86:
REFERENCE/POCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-777-9257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       finear
: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 50.9
Best Local Similarity 75.9
Matches 22; Conservative
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                                                                                                                                                                                                                                                 San Francisco
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                                                         GENERAL INFORMATION:
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S-07-947-120-9/c
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US-07-947-120-9
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Search completed: September 28, 1999, 16:41:09 Job time: 7055 sec

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                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,508
FILING DATE: 23-DEC-1993
CLASSIFICATION: 435
ATORNEZ/AGENT INFORMATION:
NAME: BENY Stephen A.
REGISTRATION UNMBER: 19,768
REFERENCE/DOCKET NUMBER: 18740/125/CACO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.4e+02
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Pred. No. 1.4e4
0; Mismatches
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                 : Floppy disk
IBM PC compatible
                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
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75.9%;
                                                                                                                                                                                                                                                TELEFAX: 202 672 5399
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 1820 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 75.9
Matches 22: Conservative
OMPUTER READABLE FORM:
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LOCATION:
FEATURE:
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FEATURE:
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W63911 404 bp mRNA EST 10-JUN-1996 md90ell.rl Scares mouse embryo NDWE13.5 14.5 Mus musculus cDNA clone IMAGE:385294 5', mRNA sequence. 91371469 W63911.1 555...58... Score LOCUS ACCESSION NID VERSION RESULT 1 W63911/c Result No. 000000 8 ; Search time 2095.87 Seconds (without alignments) 32.940 Million cell updates/sec GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd. agetggegeeteeegggeggategggageeae 2546578 segs, 986266752 residues September 28, 1999, 15:38:38 nucleic search, using sw model US-09-037-657-30 em_est19: gb_est1:* em_est10 em_est18 em_est1:* em_est11 gb_est10 gb_est16 gb_est18 em_est2: em_est3: em_est4: em_est5: em_est6: em_est7: em_est8: em_est8: em_est13 gb_est8: gb_est12 gb_est13 _est14 gb_est15 gb_est20 gb_est24 gb_est9 gb_est11 IDENTITY_NUC gb_est2 gb_est3 gb_est4 gb_est6 est2 em_est1 em_est1 gb_est5 gb_est2 gb_est7 Title: Perfect score: Sequence: Scoring table: nucleic Searched: Database Run on:

T31953 EST41425 HU W57897 zd17d12.s1 AA042972 zk56d06.r

AA091923

nr35g12. GM02819.

AA635631 AA695430 AA695938

AA391856 AA392321

AA201099 AA275781 AA04297

ALIGNMENTS

GI:1371469

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AA052662 mf41c04.r
AA102248 mp45h11.r
AA116255 mg06e12.r
AA124665 mp79e08.r
AA518890 v102h06.r
AA691737 vs12f12.r
AA8931 aL600908.s
W74180 zd75e07.s1
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A1197884 q148901.x
A1355982 ac914017.x
A1355982 ac914017.x
A135255 tg09c07.x
A1401119 tg26b06.x
A1470829 t189f02.x
A1640129 wa29e01.x
A1640362 wa17402.x
W46604 zc32h10.s1
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AA555903 nm65903.8
AA622624 np55f03.8
AA091921 nm1518.se
AA880407 vx40001.r
AI575060 UT.R-G0-u
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C74272 C74272 Rice
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W82073 me96f06.r1
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AI574687 UI-R-GO
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T84586 yd50d04.r1
W30648 mc14d08.r1
                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                            Description
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W82073
AA052662
AA105248
AA116255
AA124665
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em_est22:*
em_est23:*
em_est24:*
em_est25:*
em_est25:*
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                                                                                                                                                                                                   Query
Match 1
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ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

FEATURES

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T 3'), on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Uniu., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library went through one round of
DTMAILSTATION, and was constructed by Bento Soares and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases i to 814)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/Mouse EST Project
WashU-HMIM Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parky School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: mouseest@watson.wustl.edu
Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:247195
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .834
/organism="Mus musculus"
/organism="C57BL/6J"
/db_xref="taxon:10090"
/clone="IRAGE:403427"
/clone="Ib="soares mouse embryo NbME13.5 14.5"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 834;
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/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 26;
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%
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High quality sequence stop: 476.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 22.2; DF
Pred. No. 83;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 agctggcgcctcccgggcggatcgggagcccac 35
                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston, R.
The WashU-HHMI Mouse ESI Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M.Fatima Bonaldo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1996)
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Best Local Similarity 77.1'
Matches 27; Conservative
                                                Mus musculus
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AAO52662/c
LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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ORIGIN
                                            ORGANISM
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JOURNAL
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AUTHORS
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SOURCE
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14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Uniu., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacla), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library went through one round of
mormalization, and was constructed by Bento Soares and
M.Fatima Bonaldo. 93 t
                                                                                                                                                                 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

[ (bases 1 to 404)
] Marrah, Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pT7T3D-Pac (Pharmacia) with a modified bobylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' reflace with a Not II - oligo(dT) primer [5' reflace with a Not II - oligo(dT) primer [5' reflace with a Not II - oligo(dT) primer [5' reflace with a Not II - oligo(dT) primer [5' reflace with a Not II - oligo(dT) primer [5' reflace with a Not II - oligo(dT) primer [5' reflace with a world with a Not II - oligo(dT) primer [5' reflace with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world with a world wit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
WashD-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
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me96f06.rl Scares mouse embryo NbME13.5 14.5 Mus musculus cDNA
clone IMAGE:403427 5', mRNA sequence.
                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU HHMI Mouse EST Project
Unpublished (1996)
On May 9, 1995 this sequence version replaced gi:802631
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/clone_lib="Soares mouse embryo NDMEl3.5 14.5"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26; Length 404;
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/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 agctggcgcctcccgggcggatcgggagcccac 35
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/map="19"
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W82073.1 GI:1393024
EST.
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1 Similarity 77.1%;
27; Conservative C
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Gaps

Query Match

Matches

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BASE COUNT ORIGIN

DEFINITION

ACCESSION

VERSION KEYWORDS

RESULT 2 W82073/c LOCUS

TITLE JOURNAL COMMENT

FEATURES

REFERENCE

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/clone="IMAGE:572229"
/clone_lib="Barstead MPLRB1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism-"Mus musculus"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref-"taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Kidney"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="6 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="BALB/c'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91671348
AA116255.1 GI:1671348
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Best Local Similarity 77.17
Watches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 256)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T 3'), on equal amounts of mRNA from 2 13.5dpc and 2 state Univ. from 2 ]; double-stranded cDNA was ligated to ECO RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and ECO RI sites of the modified normalization, and was constructed by Bento Soares and M.Fatima Bonaido. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA105248 341 bp mRNA EST 13-FEB-1997 mP45h11.r1 Barstead MPLRB1 Mus musculus cDNA clone IMAGE:572229 5',
                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 341)
                                                                                                                                The WashU-HHMI Mouse EST Project
Unpublished (1996)
On May 8, 1995 this sequence version replaced gi:800265.
                                                                                                                                                                                                               Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_lib="Soares mouse embryo NbME13.5 14.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
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8
                                                                                                                                                                                                                                                                                                                                                                                                          Seg primer: -28M13 rev2 from Amersham
High quality sequence stop: 81.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.4%; Score 22.2; DB 77.1%; Pred. No. 69; Live 0; Mismatches
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    .256
    /organism="Mus musculus"

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/clone="IMAGE:407622"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M.Fatima Bonaldo
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AA105248
                                                                                                                  Waterston, R
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Matches 27; Conser
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AA105248/c
LOCUS
DEFINITION
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BASE COUNT ORIGIN

ô 윱 ORGANISM

REFERENCE

ACCESSION

VERSION SOURCE

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Dubuque, T.,
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:346877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA116255 441 bp. mRNA EST 17-FEB-1997 mq06e12.rl Soares 2NDMT Mus musculus cDNA clone IMAGE:577966 similar to TR:6203113 G203113 BETA'-CHAIN CLATHRIN ASSOCIATED PROTEIN COMPLEX AP-1. ;, mRNA sequence.
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J.; Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                          Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced g1:1282726.
                                                                                                                                                                                                                                           Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseestewatson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: -28m13 rev2 ET from Amersham
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Contact: Marra M.Mouse EST Project
WashU-HMM Mouse EST Project
WashU-HMM MO 63108
#444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
#444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
#413 14 286 1800
Fax: 314 286 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 22.2; DB 29;
Pred. No. 77;
0; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="IMAGE:575462"
/clone_lib="Soares 2NbMT"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
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AA518890.1 GI:2259433
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illarity 77.1%;
Conservative
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Best Local Similarity
Matches 27; Conserva
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AA518890/c
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                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:352614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA124665 525 bp mRNA EST 17-FEB-1997 mp79e08.r1 Soares 2NbHT Mus musculus cDNA clone IMAGE:575462 5' similar to TR:6203113 G203113 BFTA'-CHAIN CLATHRIN ASSOCIATED PROTEIN COMPLEX AP-1. ; mRNA sequence.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 525)
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On Sep 12, 1996 this sequence version replaced g1:1290543.
                                                   On Sep 12, 1996 this sequence version replaced g1:1293995.
                                                                                                                             WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tal: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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High quality sequence stop: 435.
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Pred. No. 75;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 .441
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:577966"
/clone_lib="Soares 2NbMT"
                                                                                                  Contact: Marra M/Mouse EST Project
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The WashU-HHMI Mouse EST Project
  The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
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Best Local Similarity 77.1%;
Matches 27; Conservative
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                        Unpublished
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AA124665/c
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Length 525; Indels

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 423)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsells.T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moorie,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                    AA518890 423 bp mRNA EST 16-JUL-1997 v102h06.rl Barstead mouse myotubes WPLRB5 Mus musculus cDNA clone IMAGE:902651 5' similar to TR:G203113 G203113 BETA'-CHAIN CLATHRIN ASSOCIATED PROTEIN COMPLEX AP-1.;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Sep 12, 1996 this sequence version replaced gi:1397524
236 Arcagegaeccrccreegreerrcagaecccac 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
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The WashU-HHMI Mouse EST Project
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B
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                                                                                                                                                                                                                                                                                                                                                                                                                     3'); double-stranded CDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified p7713 vector. Library constructed by Bob Barstead. The C2c12 cell line (available from ATC, catalog # CRL-1772) differentiates rapidly, forming contractile myotubes and producing characteristic muscle proteins.
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Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                             Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL; contact the INAGE Consortium (info@kmage.llnl.gov) for further information.
Seq primer: -28ml3 xev2 Er from Amersham.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Unpublished (1996)
On Sep 12, 1996 this sequence version replaced g1:1393359.
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 34; Length 423;
                                                                                                                                                                                                                                                                /clone="IMAGE: 902651"
/clone_lib="Barstead mouse myotubes MPLRB5"
/cell_line="C2C12"
/lab_host="DH108"
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Pred. No. 75;
0; Mismatches
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                                                                                                                                                                                                               /organism="Mus musculus"
/strain="C3H"
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Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                    /db_xref-"taxon:10090"
                                                                                                                                                                        Location/Qualifiers
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77.1%;
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Best Local Similarity 77.1'
Matches 27; Conservative
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AA691737/c
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AUTHORS
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JOURNAL
COMMENT
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KEYWORDS
SOURCE
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al60g08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1461758 3' similar to contains Alu repetitive element;, mRNA
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 473)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:61939 Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
INSERT Length: 597 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 470.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                            /clone_lib="Barstead mouse irradiated colon MPLRB7"
/dev_stage="8 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Jan 14, 1998 this sequence version replaced gi:1798628.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 346;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 22.2; DB 37;
Pred. No. 73;
0; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 agctggcgcctcccgggcggatcgggagccac 35
                                                                                                                                                     'organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="21"
                                                                                                                                                                            /strain="FVB/N"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                            /clone="IMAGE:1138127"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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Best Local Similarity 77.1
Matches 27; Conservative
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Jnpublished (1997)
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KEYWORDS
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COMMENT
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                                    /ncce="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_GAP_CGBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CONAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297486-332087, 682632-687239, 726408-72871, and 729096-731399. Subtraction by Bento Soares and M. Patima Bonaldo.
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/dev_stage="19 weeks"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: heart; Vector: pT773D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 575 Std Error: 0.00
Seq primer: mob.REGA+ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W74180 435 bp mRNA EST 17-0CT-1996 zd75e07.s1 Soares_fetal_heart_NDHH19W Homo sapiens cDNA clone IMAGE:346500 3', mRNA sequence.
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rikkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarhini; Hominidae; Homo.
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On Nov 29, 1993 this sequence version replaced gi:430390.
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                                                                                                                                                                                                                                                                                                                                                                                               Query Match 60.6%; Score 21.2; DB 39; Best Local Similarity 76.5%; Pred. No. 1.6e+02; Matches 26; Conservative 0; Mismatches 8;
    /clone_lib="Soares_NFL_T_GBC_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364 GCTGGCGCCCTCCCGTGCCCATGGGGAGAGAC 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 gotggcgcgctcccgggcggatcgggagcccac 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="GDB:1271875"
/db_xref="taxon:9606"
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Location/Qualifiers
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W74180.1
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DEFINITION
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W74180
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DRIGIN
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AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 447)
NCI-CGAP http://www.ncbl.nlm.nih.gov/nclogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length; 715 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                   AI191353 447 bp mRNA EST 29-OCT-1998 qe32c09.s1 Soares_fetal_lung_NbHL19W Homo sapiens CDNA clone IMAGE:1740688 3', mRNA sequence.
                                                                                                        Gaps
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Unpublished (1997)
On May 8, 1995 this sequence version replaced g1:801250.
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                                                                   Score 21; DB 26; Length 435;
Pred. No. 1.9e+02;
0; Mismatches 5; Indels
 4 others
 104 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nlh.gov
                                                                                                                                                                        377 GETGGCGCCCTCCCGTGCCCATGGGGAG 405
                                                                                                                                          2 gctggcgccctcccgggcggatcgggag 30
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117 9
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g3742562
A1191353.1 GI:3742562
                                                                     Query Match
Best Local Similarity 82.8%;
Matches 24; Conservative (
 131 c
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RESULT 12 AI574687

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DEFINITION

ACCESSION

NID VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL MEDLINE COMMENT

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University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA 7e1: 319 335 8250
Fax: 319 335 8250
Email: msoarces@blue.weeg.utowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soarces Lab Clone distribution: clones will be available through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anote—"Vector: pTTT3D-Pec (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco Ri; The UI-R-GO library is a normalized library constructed from a mixture of rat tissues (nodose ganglia, dorsal root ganglia, and trigeminal ganglia). The tag is a string of nucleotides present between the Not I site and the oligo-dT track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6:
                                                                                                                                                                                                                                                                                                                                                                         Raftus norvegicus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 332)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                            J32 bp mRNA EST 05-APR-1999 UI-R-GO-ut-h-08-0-UI.83 UI-R-GO Rattus norvegicus CDNA clone AI579568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Mar 10, 1998 this sequence version replaced g1:2948398.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 20.2; DB 48;
Pred. No. 3.3e+02;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="UI-R-G0-ut-h-08-0-UI"
/clone_11b="UI-R-G0"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Research Genetics (www.resgen.com)
Seq primer: M13 Forward,
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97044477
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/db_xref="taxon:10116"
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75.8%;
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AI579568
                                                                                                                   LOCUS
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ORGANISM
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C74272
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AUTHORS
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MEDLINE
COMMENT
                                                                                                                                                                                                                     ACCESSION
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                                                                                                                                                                                                                                                                                VERSION
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                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Sescarch Genetics (www.resgen.com)
Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mixture of rat tissues (nodose ganglia, dorsal root ganglia, and trigeminal ganglia). The tag is a string of oncleotides present between the Not I site and the oligo-dr track. The library was constructed as described by Bonaldo, Lennon and Soares.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 319)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA 7e1: 319 335 9250 Fax: 319 335 9565 Eax: 319 335 9565 Eax: 319 335 9565
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/lab_host="bH10B (Life Technologies)"
/note="vector: pT73D-Pac (Pharmacla) with a modified polylinker; Site_1: Not I; Site_2: Eco R; The UI-R-GO library is a normalized library constructed from a mixture of rat tissues (nodose ganglia, dorsal rooting in the constructed from a second construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the con
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                               AI574687 319 bp mRNA EST 30-MAR-1999
UI-R-GO-uc-b-11-0-UI.s1 UI-R-GO Rattus norvegicus CDNA clone
UI-R-GO-uc-b-11-0-UI.3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On May 18, 1998 this sequence version replaced gi:3138307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                   Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
ch 60.0%; Score 21; DB 43; L4 Similarity 82.8%; Pred. No. 1.9e+02; 24; Conservative 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 20.2; DB 48;
Pred. No. 3.3e+02;
0; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                map="6p21.3; 5q33"
clone="UI-R-GO-uc-b-11-0-UI"
clone_lib="UI-R-GO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Rattus norvegicus"
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97044477
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/db_xref="taxon:10116"
/map="6p21.3; 5q33"
                                                                                                                                                             351 GCTGGCGCCCTCCCGTGCCCATGGGGAG 379
                                                                                                                                      30
                                                                                                                         2 gctggcgcgctcccgggcggatcgggag
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AI574687.1 GI:4544683
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llarity 75.8%;
Conservative (
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Query Match
Best Local Similarity
Matches 24; Conserv
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Best Local Similarity
Matches 25; Conserv
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FEATURES

BASE COUNT ORIGIN

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Gaps

us-09-037-657-30.rst

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Query Match
Best Local Similarity
Matches 24; Conserv
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ORIGIN
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CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209 bp mRNA .EST 27-AUG-1998 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1641667 to contains MER22.t3 MER22 repetitive element ;, mRNA
                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 209)
NCI-CGAP http://www.ncbl.nlm.nih.gov/nciogap.
NCI-CGAP http://www.ncbl.nlm.nih.gov/nciogap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Unpublished (1997)
On Nov 29, 1993 this sequence version replaced gi:636002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                   On May 8, 1995 this sequence version replaced g1:801536.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.6%; Score 19.8; DB 36; Length 335; ilarity 75.0%; Pred. No. 4.5e+02; Conservative 0; Mismatches 8; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:4530"
/clone="E30775_4A"
/clone="1b="Rice panicle shorter than 3cm"
/close_stage="shorter than 3cm"
/note="Grgan: panicle"
105 c 100 g 60 t 14 others
                                                                                                                                                                                                                                                                     National Institute of Agrobiological Resources
Rice Genome Research Program
2-1-2 Kannondai, Tsukuba
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .335
/organism="Oryza sativa'
                                                                                                                                                                                                                                                                                                                                                        Japan 305
Tel: 0298-38-7441
Fax: 0298-38-7468
Email: tsasaki@abr.affrc.go.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="Nipponbare
                                                                                                                                                     Sasaki,T. and Yamamoto,K.
Rice cDNA from panicle
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI016400.1 GI:3230736
                                                                                                                                                                                                                                                        Contact: Takuji Sasaki
C74272.1 GI:2442501
                                                                                                                                  (bases 1 to 335)
                                                                                                                  Poaceae; Oryza.
                                       Oryza sativa.
Oryza sativa
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Matches 24; Conserv
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ov59h10.s1 8
3' similar t
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KEYWORDS
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ORGANISM
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NID
                                                        ORGANISM
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AUTHORS
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AUTHORS
TITLE
JOURNAL
COMMENT
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VERSION
KEYWORDS
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/note-"Vector: pT713D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mNNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                          Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 209;
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found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 19.8; DB 41;
Pred. No: 4.2e+02;
); Mismatches 7;
                                                            Insert Length: 349 Std Error: 0.00
Seg primer: -40ml3 fwd. ET from Amersham
Location/Qualifiers
                                                                                                                                                                                                       /clone="IMAGE:1641667"
/clone=lib="Soares_testis_NHT"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: September 28, 1999, 15:38:41 Job time: 3309 sec
                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.6%;
nilarity 77.4%;
Conservative 0
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